

Result No.	Score	Query Match	Length	DB ID	Description
1	84	100	0	427 1 KGHUL1	kininogen, LMW pre-kininogen, HMW pre-kininogen, HMW I
2	84	100	0	644 1 KGHUH1	K-kininogen, LMW I
3	67	79	8	433 2 A28055	kininogen, HMW I P
4	67	79	8	639 2 A25486	kininogen, HMW II
5	59	70	2	434 1 KGBOL2	kininogen, HMW II
6	59	70	2	619 1 KGOBH2	major acute phase T-kininogen I prec
7	56	66	7	423 1 KGRTM1	major acute phase T-kininogen, HMW I
8	56	66	7	430 1 KGRTP1	hypothetical proteo
9	56	66	7	430 2 A23897	Nuc-2 protein - N
10	56	66	7	430 2 B28055	TPR-repeat-contain
11	54	64	3	436 1 KGBOL1	hypothetical proteo
12	54	64	3	621 1 KGOBH2	hypothetical proteo
13	43	51	2	217 2 B97948	protein F3M18.12 [
14	43	51	2	466 1 AH1213	FN916 ORF1 homolo
15	42	50	0	657 2 BB4791	hypothetical proteo
16	41.5	49	4	469 2 F69403	hypothetical proteo
17	41	48	8	454 2 G75105	hypothetical proteo
18	41	48	8	895 2 T23191	hypothetical proteo
19	41	48	8	996 2 F86410	protein F3M18.12 [
20	41	48	8	1007 2 F32285	hypothetical proteo
21	41	48	8	1066 2 S72479	Nuc-2 protein - N
22	40.5	48	2	346 2 B97014	TPR-repeat-contain
23	40	47	6	85 2 C90097	hypothetical proteo
24	40	47	6	179 2 A48474	ICP18.5 homolog -
25	40	47	6	313 2 E81356	hypothetical proteo
26	40	47	6	323 2 S7103	hypothetical proteo
27	40	47	6	388 2 C95102	hypothetical proteo
28	40	47	6	388 2 E97970	hypothetical proteo
29	40	47	6	431 2 F89817	conserved hypothet

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:37 ; Search time 18 Seconds
(without alignments)

85.453 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATFYFKIDNVKKAR 16

Scoring table: BLOSSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28324 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1

KGHUL1
Kininogen, LMW precursor [validated] - human
N; Alternate names: alpha-2-thiol proteinase inhibitor; Preprokininogen
N; Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C; Species: Homo sapiens (man)
C; Date: 06-Jul-1982 #sequence_change 08-Dec-2000
C; Accession: A01280; B22276; A27900; A27699; A34030
R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiozaki, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
A; Reference number: A90490; MUID:85122621; PMID:6441591
A; Accession: A01280
A; Molecule type: mRNA
A; Residues: 1-427 <ORF>
A; Cross-references: GB:ML11437; NID:9186751; PIDN:AAB59551.1; PID:9386853
R; Lottspeich, F.; Kellermann, J.; Rauth, G.; Mueller-Esterl, W.
in Kinins IV, Part A, Greenbaum, L.M., and Margolius, H.S., eds., pp. 91-95. Plenum, N
A; Title: Amino acid sequence of the light chain of human low molecular mass kininogen
A; Reference number: A27900
A; Accession: A27900
A; Molecule type: protein
A; Residues: 1-427 <ORF>
R; Mardroiu, T.; Carretero, O.A.; Proust, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin moiety in human plasma kininogens.
A; Reference number: A27900
A; Accession: A27900
A; Molecule type: protein
A; Residues: 380-389 <MIN>
R; Maeda, H.; Matsunura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A; Title: Purification and identification of [hydroxyprolyl(3)-18Syl-bradykinin in ascitic f
A; Reference number: A31905; MUID:8820921; PMID:3365237
A; Accession: A31905
A; Molecule type: protein
A; Residues: 381-389 <MAX>
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A; Title: Identification of [hydroxyproline(3)-18Syl-bradykinin released from human p
A; Reference number: A34030
A; Accession: A34030
A; Molecule type: protein
A; Residues: 380-389 <SAS>

R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S. J. Biol. Chem. 260, 8610-8617, 1985
 A;Title: Structural organization of the human kininogen gene and a model for its evolution
 R;Pierce, J.V.
 A;Contents: annotation: bradykinin
 A;Reference number: A93545; MUID:85224583; PMID:2989294

A;Title: Structural features of plasma kinins and kininogens.
 A;Reference number: A91455; MUID:90255622; PMID:4955632
 C;Comment: The LMW kininogen precursor is produced from the same gene as the HMW form (s)
 C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the
 xiproxiprant residue is present in the kininogen prior to the release of bradykinin.
 C;Genetics:

A;Gene: GDB:RNG
 A;Cross-references: GDB:125256; OMIM:228960
 A;Map position: 3q27-3q27
 A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3; 401/3
 C;Superfamily: kininogen; cystatin homology
 C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glycine
 F;19-4-27/Product: LMW prokininogen (kininogen I) #status predicted <SIG>
 F;19-389/390-427/Product: LMW kininogen II #status predicted <MAT>
 F;19-379/390/Product: LMW kininogen heavy chain #status predicted <HCII>
 F;19-131/Domain: cystatin homology <CY1>
 F;142-253/Domain: cystatin homology <CY2>
 F;264-315/Domain: cystatin homology <CY3>
 F;380-389/Product: lysyl-bradykinin (kallidin III) #status experimental <BDY>
 F;381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
 F;390-427/Product: LMW kininogen light chain #status experimental <LCII>
 F;19/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted
 F;48-119,205/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
 F;383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F;401/Binding site: carbohydrate (Thr) (covalent) #status absent

Query Match Score 100.0%
 Best Local Similarity 100.0%
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATYFKEIDVKKAR 16
 ||||| ||||| ||||| |||||
 Db 293 NNATYFKEIDVKKAR 308

RESULT 2
 KGHUH1
 Kininogen, HMW precursor [validated] - human
 N;Alternate names: alpha-2-thioli proteinase inhibitor; preprokininogen; prokininogen
 N;Contains: bradykinin (kallidin 1); HMW kininogen I; HMW kininogen II; low molecular weight
 C;Species: Homo sapiens (man)
 C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000
 C;Accession: A01279; A25216; S32422; A91153; A24871; A27899; A31905; A34030; S02
 R;Okuhiko, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
 Biochimica et Biophysica Acta, 23, 5691-5697, 1994
 A;Title: Isolation of a human cDNA for alpha-2-thioli proteinase inhibitor and its identification
 A;Reference number: A90490; MUID:85122621; PMID:6441591
 R;Accession: A01279
 A;Molecule type: mRNA
 A;Residues: 1-389 <ORF>

R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
 A;Reference number: A92544; MUID:2989293
 R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfaig-Machleidt, I.
 A;Molecule type: mRNA
 A;Residues: 1-592, 'I', 594-644 <TAK>
 A;Cross-references: GB:MI1437; NID:9186751; PIDN:AAB59550-1; PID:9386852
 R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfaig-Machleidt, I.
 A;Molecule type: protein

FEBS Lett. 321, 93-97, 1993
 A;Title: Cloning, expression and characterization of human kininogen domain 3.
 A;Reference number: S32422; MUID:93223854; PMID:8467916
 A;Accession: S32422
 A;Molecule type: mRNA
 A;Residues: <ANS>; 253-377 <AUE>
 A;Note: differences are due to known cloning artifacts
 R;Lottspeich, F.; Kellermann, J.; Henschien, A.; Foertsch, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A;Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen
 A;Reference number: A91153; MUID:86030270; PMID:4054110
 A;Accession: A91153
 A;Molecule type: protein
 A;Residues: 379-644 <LOT>
 A;Note: the bradykinin sequence preceding the light chain sequence was not determined
 R;Kellermann, J.; Lottspeich, F.; Henschien, A.; Mueller-Esterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A;Title: Completion of the primary structure of human high-molecular-mass kininogen.
 A;Reference number: A24871; MUID:86108361; PMID:3484703
 A;Accession: A24871
 A;Molecule type: Protein
 A;Residues: 'Z', 20-380 <KEIL2>
 R;Kellermann, J.; Lottspeich, F.; Henschien, A.; Mueller-Esterl, W.
 In Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New York, 1986
 A;Title: Amino acid sequence of the light chain of human high molecular mass kininogen
 A;Reference number: A27899
 A;Accession: A27899
 A;Molecule type: Protein
 A;Residues: 379-389 'K' 390-407, 'Q', 409-644 <KEIL2>
 R;Mindruo, T.; Carretero, O.A.; Prod'ho, D.; Walz, D.; Scicli, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A;Title: A new kinin moiety in human plasma kininogens
 A;Reference number: A27699; MUID:88209021; PMID:3355237
 A;Accession: A27699
 A;Molecule type: protein
 A;Residues: 380-389 <MIN>
 R;Maeda, H.; Matsumura, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic fluid
 A;Reference number: A31905; MUID:89034061; PMID:3182782
 A;Accession: A31905
 A;Molecule type: protein
 A;Residues: 381-389 <MAE>
 R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A;Title: Identification of [hydroxyprolyl(3)]-Iyyyl-bradykinin released from human platelets
 A;Reference number: A34030; MUID:88106632; PMID:3337729
 A;Accession: A34030
 A;Molecule type: protein
 A;Residues: 380-389 <SA5>
 R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorot, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A;Title: Human cathepsin B and cysteine proteinase inhibitors (CPIS) in inflammatory diseases
 A;Reference number: S02482; MUID:89076517; PMID:3264507
 A;Accession: S02482
 A;Molecule type: Protein
 A;Residues: 1-19; 189-192; 310-314; 381-389 <LEN1>
 R;Kato, H.; Matsumura, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A;Title: Isolation and identification of hydroxyproline analogues of bradykinin in human platelets
 A;Reference number: A61495; MUID:88211869; PMID:3366244
 A;Accession: A61495
 A;Molecule type: protein
 A;Residues: 380-389 <KAT>
 A;Experimental source: urine
 A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A;Accession: B61495
 A;Molecule type: protein
 A;Residues: 381-389 <KAT>
 A;Experimental source: urine
 A;Note: this peptide had Pro-383 modified to 4-hydroxyproline
 A;Accession: C61495
 A;Molecule type: protein

A;Residues: 380-389 <KAT3>
 R;Lenarcic, B.; Krasovce, M.; Ritonja, A.; Olafsson, I.; Turk, V.
 A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
 A;Accession number: S14303; PMID:2013314
 A;Molecule type: protein
 A;Residues: 264-359,'N',361-375 <LEN2>
 R;Little, S.S.; Johnson, D.A.
 Blochim. J. 307, 341-346, 1995
 A;Title: Human mast cell trypsinase isoforms: separation and examination of substrate-specificity
 A;Reference number: S55239; PMID:95251593; PMID:7733867
 A;Molecule type: protein
 A;Residues: 450-452,'X',454,'X',456 <LEN2>
 R;Strazcek, F.; Maachi, F.; Nguyen, D.; Becciu, M.; Heulin, M.H.; Nabet, P.; Belleville, J. Biol. Chem. 273, 207-211, 1995
 A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like growth factor-I receptor activity
 A;Accession number: A92245; PMID:7589467
 A;Contents: annotation; gene organization
 R;Pierce, J.V.
 Fed. Proc. 27, 52-57, 1968
 A;Title: Structural features of plasma kinins and kininogens.
 A;Accession number: A91455; PMID:90255622; PMID:4952632
 A;Contents: annotation; bradykinin
 C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene by alternative splicing.
 C;Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the Hageman factor cascade and is involved in blood coagulation.
 C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is important for its biological activity.
 C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, hypotensive and antidiuretic.
 C;Genetics:
 A;Gene: GDB:KNG
 A;Cross-references: GDB:125256; OMIM:228960
 A;Pdb position: 3927-3927
 A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
 C;Superfamily: kininogen; cystatin homology
 C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication; signal sequence; status experimental <SIG>
 F:1-18/Domain: signal sequence #status experimental <SIG>
 F:19-379/Domain: HMW kininogen II #status experimental <MAT2>
 F:19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
 F:19-379/Domain: cystatin homology <CY1>
 F:19-379/Domain: cystatin homology <CY2>
 F:19-379/Domain: cystatin homology <CY3>
 F:19-379/Domain: lysyl-bradykinin (kallidin II) #status experimental <RBDY>
 F:381-389/Domain: bradykinin (kallidin I) #status experimental <BYD>
 F:390-644/Domain: HMW kininogen light chain #status experimental <LCH>
 F:42-510/Region: glycine/histidine/lysine-rich 30-residue repeats
 F:431-434/Product: low molecular weight growth promoting factor #status experimental <GP>
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental <GP>
 F:26-614,83-94,107-126,142-145,206-218,248,264-267,328-340,351-370/disulfide bonds:
 F:41/Binding site: carbohydrate (Asn) (covalent) #status absent
 F:169,205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental
 F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
 F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
 F:401,531,542,546,557,571,591,628/Carbohydrate (Thr) (covalent) #status experimental
 F:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 84; DB 1; Length 64;
 Best Local Similarity 100.0%; Pred. No. 4.2e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDNVKK 16
 Db 293 NNATFYFKIDNVKK 308

RESULT 3
 A28055
 K-kininogen, LMW I precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 15-Nov-1996
 C;Accession: A28055
 R;Puturo-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 12054-12059, 1985
 A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin inhibitor.
 A;Reference number: A92496; MUID:86008264; PMID:2413018
 A;Accession: A28055
 A;Molecule type: mRNA
 A;Residues: 1-433 <FUR>
 C;Superfamily: kininogen; cystatin homology
 C;Keywords: alternative splicing
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-433/Product: K-kininogen, LMW I #status predicted <MAT>
 F:19-131/Domain: cystatin homology <CY1>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CY3>

Query Match 79.8%; Score 67; DB 2; Length 433;
 Best Local Similarity 86.7%; Pred. No. 0.002; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 NNATFYFKIDNVKK 15
 Db 293 NNATFYFKIDNVKK 307

RESULT 4
 A25486
 K-kininogen, HMW I precursor - rat
 N;Contains: bradykinin
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
 R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 262, 2190-2196, 1987
 A;Title: Differing expression patterns and evolution of the rat kininogen gene family
 A;Reference number: A92625; MUID:87137443; PMID:3029068
 A;Accession: A25486
 A;Molecule type: mRNA
 A;Residues: 1-639 <KIT>
 A;Note: The authors translated the codon CAA for residue 347 as Asn
 C;Keywords: alpha-2-thiol proteinase inhibitor
 F:1-18/Domain: signal sequence #status predicted <SIG>
 C;Superfamily: kininogen; cystatin homology
 C;Keywords: alternative splicing
 F:1-18/Domain: kininogen, HMW I #status predicted <MAT>
 F:19-131/Domain: cystatin homology <CY1>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CY3>

Query Match 79.8%; Score 67; DB 2; Length 639;
 Best Local Similarity 86.7%; Pred. No. 0.0029; Mismatches 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDNVKK 15
 Db 293 NNATFYFKIDNVKK 307

RESULT 5
 KG012
 kininogen, LMW II precursor - bovine
 N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
 N;Contains: bradykinin (kallidin); kininogen I; prokininogen
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-May-1999
 C;Accession: A01284

A; Residues: 1-434 <NAW>
 A; Cross references: GB:V00427; GB:J00011; NID:9489; PIDN:CAA23701; PID:9490
 C; Comment: The LMW kininogen precursor is produced from the same gene as the HMW form as
 C; Comment: Kininogen is cysteine proteinase inhibitor, takes part in initiation of the
 C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i
 C; Superfamily: kininogen; cystatin homology
 C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; glyc
 F; 1:18-/Domain: signal sequence #status predicted <SIG>
 F; 19-43-/Product: LMW kininogen II #status predicted <MAT>
 F; 19-130-/Product: LMW kininogen I heavy chain #status predicted <HCH>
 F; 141-252-/Domain: cystatin homology <CY2>
 F; 371-386-/Domain: cystatin homology <CY3>
 F; 371-386-/Product: cystein-bradykinin (kallidin III) #status predicted <KBDY>
 F; 378-386-/Product: bradykinin (kallidin I) #status predicted <BDY>
 F; 387-434-/Product: LMW kininogen I light chain #status experimental <LCH>
 F; 19-/Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted
 F; 27-404, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:
 F; 387-434-/Product: LMW kininogen I binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 376-377-/Cleavage site: Met-Lys (kallikrein) #status predicted
 F; 380-/Modified site: 4-hydroxyproline (Pro) #status predicted
 F; 386-387-/Cleavage site: Arg-Ser (kallikrein) #status predicted

Query	Match	Score	DB 1:	Length
	Best local Similarity	70.2%; 73.3%;	0.043;	34;
	Matches 11:	Conservative	2;	Mismatches 2;
			Indels 0;	Gaps 0;
Qy	1	NNATFYFIDNYRKA 15		
Ddb	290	HDGSTFYFKIDTVKKA 304		

RESULT 6

KGIOH2
 Kininogen, HMW II precursor - bovine
 NN/Alternate names; alpha-2-thiol proteinase inhibitor; preprokininogen
 N/Contbins: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
 R:Kitamura, N.; Takagishi, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakaniishi, S.
 A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and
 A;Reference number: A91923; MUTID:70180420; PMID:4986212
 A;Accession: A91923
 A;Molecule type: protein
 A;Residues: 1-619 <KTT>
 A;Cross references: GB:V01492; GB:K01758; NID:9493; PIDN:CAA24736.1; PID:9494
 R:Rat, H.; Nagasawa, S.; Suzuki, T.
 R:Ran, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
 J. Biochem. 67, 313-323, 1970
 A;Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino
 A;Reference number: A91941; MUTID:76260155; PMID:950151
 A;Accession: A91941
 A;Molecule type: protein
 A;Residues: 376-391 <KAT>
 A;Note: 398-Pro, 401-Val, and 455-Lys were also found
 R:Ran, Y.N.; Komiyama, M.; Iwanaga, S.; Suzuki, T.
 J. Biochem. 77, 55-69, 1975
 A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Ami

A;Molecule type: mRNA
A;Residues: 1-423 <COL>
C;Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflammation, bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam-
C;Keywords: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam-
C;Superfamily: kininogen; cystatin homology
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence ID: JQ0027; text_change 22-Jun-1999
C;Accession: A01286; D25486; A28576; PL0193; JQ0027; B25408; A28525; S68036
R;Furuto,Kato, S.; Matsuamoto,A.; Kitamura,N.; Nakaniishi,S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
nhibitor.
A;Reference number: A92496; PMID:86008264; PMID:2413018
A;Accession: A01286
A;Molecule type: mRNA
A;Residues: 1-430 <PUR>
A;Cross References: GB: M11883; PID:9205084; PID:AAA41489_1; PID:9205085
R;Kitagawa,H.; Kitamura,N.; Hayashida,H.; Miyata,T.; Nakaniishi,S.
J. Biol. Chem. 262, 2190-2196, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:8713443; PMID:3029068
A;Accession: D25486
A;Molecule type: DNA
A;Residues: 375-430 <KTR>
A;Reference number: A92729; MUID:8808726; PMID:3121623
A;Title: Purification and characterization of rat T-kininogens isolated from plasma of a
J. Biol. Chem. 263, 973-979, 1988
A;Accession: A28526
A;Molecule type: protein
A;Residues: 1-20-48; 376-430 <ENJ>
R;Kanda,S.; Sugiyama,K.; Takahashi,M.; Shumiya,S.; Tomino,S.; Nagase,S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A;Title: Identification of a protein increasing in serum of Nagase anabuminemic rats be-
A;Reference number: PL0193; MUID:90216390; PMID:2108948
A;Accession: PL0193
A;Molecule type: mRNA
A;Residues: 330-420, 'R', 422-429, 'P' <KAN>
R;Anderson,K.P.; Croyle,M.L.; Lingrel,J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding rat T-kininogen.
A;Reference number: JQ0027; MUID:90034172; PMID:2806908
A;Accession: JQ0027
A;Molecule type: DNA
A;Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258-38
A;Experimental source: strain Sprague-Dawley
R;Rageyana,R.; Kitamura,N.; Ohkubo,H.; Nakaniishi,S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation sites of rat K and

A;Reference number: A25486; MUID:87137465; PMID:3818598
A;Accession: B25488
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-48 <KAG>
A;Cross References: GB: M14356; PID:9205090; PIDN:AAA41492_1; PID:g205091
R;Enjoji,K.; Kato,H.; Hayashi,I.; Ohishi,S.; Iwanaga,S.
J. Biol. Chem. 263, 965-972, 1988
A;Title: Purification and characterization of two kinds of low molecular weight kinin
A;Reference number: A28525
A;Accession: A28525
A;Molecule type: protein
A;Residues: 376-430 <ENJ>
R;Steria,P.; Walter,R.; Vautravers,P.; Guiroz,Y.
Arch. Biochem. Biophys. 322, 333-338, 1995
A;Title: Identification of several isoforms of T-kininogen expressed in the liver of
A;Reference number: S68034; MUID:96032652; PMID:7574705
A;Accession: S68036
A;Molecule type: mRNA
A;Residues: 340-430 <SIE>
A;Experimental source: clone PSG17
C;Comment: At least three types of LMW kininogen precursors are present in rat plasma
ceding bradykinin.
C;Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after
d of an Arg or Lys, it is probably not released from its precursor by either tissue
C;Comment: The T-kininogens are produced in response to an inflammatory stimulant.
C;Genetics:
A;Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3
C;Superfamily: kininogen; cystatin homology
C;Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glyc-
F;1-18 /Domain: signal sequence predicted <SIG>
F;19-430 /Product: T-kininogen I #status experimental <MAT>
F;19-130 /Domain: cystatin homology <CYL>
F;14-1-252 /Domain: cystatin homology <CY2>
F;265-374 /Domain: cystatin homology <CY3>
F;378-386 /Product: bradykinin #status predicted <BDY>
F;19 /Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status predicted
F;82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;83,94,107-125,141-144,205-217,228-247,263-266,327-339,355-369/Disulfide bonds: #sta
Query Match Score 56; DB 1; Length 423;
Best Local Similarity 73.3%; Pred. No. 0.13%; Mismatches 3; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Query 1 NNATFYFKIDNVKKA 15
Db 285 HNHIFYFKIDTVKKA 299

RESULT 8
KGRT1
T-kininogen I precursor - rat
N;Alternative name: 73K protein; LMW kininogen T-I
N;Contains: bradykinin; T-kinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence ID: JQ0027; text_change 22-Jun-1999
C;Accession: A01286; D25486; A28576; PL0193; JQ0027; B25408; A28525; S68036
R;Furuto,Kato, S.; Matsuamoto,A.; Kitamura,N.; Nakaniishi,S.
J. Biol. Chem. 260, 12054-12059, 1985
A;Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
nhibitor.
A;Reference number: A92496; PMID:86008264; PMID:2413018
A;Accession: A01286
A;Molecule type: mRNA
A;Residues: 1-430 <PUR>
A;Cross References: GB: M11883; PID:9205084; PID:AAA41489_1; PID:9205085
R;Kitagawa,H.; Kitamura,N.; Hayashida,H.; Miyata,T.; Nakaniishi,S.
J. Biol. Chem. 262, 2190-2196, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:8713443; PMID:3029068
A;Accession: D25486
A;Molecule type: DNA
A;Residues: 375-430 <KTR>
A;Reference number: A92729; MUID:8808726; PMID:3121623
A;Title: Purification and characterization of rat T-kininogens isolated from plasma of a
J. Biol. Chem. 263, 973-979, 1988
A;Accession: A28526
A;Molecule type: protein
A;Residues: 1-20-48; 376-430 <ENJ>
R;Kanda,S.; Sugiyama,K.; Takahashi,M.; Shumiya,S.; Tomino,S.; Nagase,S.
Jpn. J. Cancer Res. 81, 63-68, 1990
A;Title: Identification of a protein increasing in serum of Nagase anabuminemic rats be-
A;Reference number: PL0193; MUID:90216390; PMID:2108948
A;Accession: PL0193
A;Molecule type: mRNA
A;Residues: 330-420, 'R', 422-429, 'P' <KAN>
R;Anderson,K.P.; Croyle,M.L.; Lingrel,J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding rat T-kininogen.
A;Reference number: JQ0027; MUID:90034172; PMID:2806908
A;Accession: JQ0027
A;Molecule type: DNA
A;Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258-38
A;Experimental source: strain Sprague-Dawley
R;Rageyana,R.; Kitamura,N.; Ohkubo,H.; Nakaniishi,S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation sites of rat K and

RESULT 9
A23897

major acute phase alpha-1 protein (version 2) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1989 #sequence ID: JQ0027; text_change 20-Aug-1999
C;Accession: A23897; B23897
R;Anderson,K.P.; Heath,E.C.
J. Biol. Chem. 260, 12055-12071, 1985
A;Title: The relationship between rat major acute phase protein and the kininogens.
A;Reference number: A23897; MUID:86008266; PMID:2413019
A;Accession: A23897
A;Molecule type: protein
A;Residues: 1-14 <AND1>
A;Accession: B23897
A;Molecule type: mRNA
A;Residues: 5-430 <AND2>
A;Cross References: GB: M11661; PID:9205307; PIDN:AAA41570_1; PMID:g205308
A;Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue
C;Superfamily: kininogen; cystatin homology
F;19-130 /Domain: cystatin homology <CYL>
F;263-374 /Domain: cystatin homology <CY3>

Query Match Score 66.7%; DB 2; Length 430;

Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3;
Indels 0; Gaps 0;

Qy 1 NNATFYFKIDIVKKA 15
Db 292 HNHLYFYFKIDIVKKA 306

RESULT 10
B28055
T-kininogen, LMW II precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Dec-1997
C:Accession: B28055; E5486; B28526; C28526
R:Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
J.Biol.Chem. 260, 12054-12059, 1985
A:Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.
A:Reference number: A92496; MUID:86008264; PMID:2413018
A:Accession: B28055
A:Molecule type: mRNA
A:Residues: 1-430 <FURS>
R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A:Title: Differing expression patterns and evolution of the rat kininogen gene family.
A:Reference number: A92625; MUID:87137443; PMID:3029068
A:Accession: E25486
A:Molecule type: DNA
A:Residues: 375-430 <KIT>
R:Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biol. Chem. 263, 973-979, 1988
A:Title: Purification and characterization of rat T-kininogens isolated from plasma of a.
A:Reference number: A92729; MUID:3121623
A:Accession: B28526
A:Molecule type: protein
A:Residues: 'E', 20-25, 'MD', 28-48, 376-430 <ENJ>
A:Accession: C28526
A:Molecule type: protein
A:Accession: 'E', 20-48, 376-388, 'R', 390-419, 'ER', 422-430 <EN2>
C:Superfamily: kininogen; cystatin homology
C:Keywords: glycoprotein; pyroglyutamic acid
F:1-18/430/Product: T-kininogen, LMW II #status predicted <SIG>
F:19-22/430/Product: T-kininogen, LMW II #status experimental <MAT>
F:19-130/Domain: cystatin homology <CY1>
F:263-374/Domain: cystatin homology <CY3>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:83-216, 204-326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:83-94, 107-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/disulfide bonds: #status

Query Match 66.7%; Score 56; DB 2; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 12

KGB0H1
kininogen, HMW I precursor - bovine
N:Alternative names: alpha-2-thiolo proteinase inhibitor; preprokininogen
N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C:Accession: A01281; A91923; A91938; A29359
R:Kitamura, N.; Togasaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.
A:Title: A single gene for bovine high molecular weight and low molecular weight kinin
A:Reference number: A93317; MUID:84014106; PMID:6571699
A:Accession: A01281
A:Molecule type: mRNA
A:Residues: 1-621 <KIT>
R:Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A:Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds a
A:Reference number: A91923; MUID:70180420; PMID:4386212
A:Accession: A91923
A:Molecule type: protein
A:Residues: 1-621 <KIT>
R:Han, Y.N.; Komiyama, M.; Iwanga, S.; Suzuki, T.
J. Biochem. 77, 55-61, 1975
A:Title: Studies on the primary structure of bovine high-molecular-weight kininogen.
A:Reference number: A91938; MUID:75170265; PMID:1169237

RESULT 11

KGB0L1
kininogen, LMW I precursor - bovine
N:Alternative names: alpha-2-thiolo proteinase inhibitor; preprokininogen
N:Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C:Accession: A01283
R:Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983
A:Title: Primary structures of bovine liver low molecular weight kininogen precursors and their
A:Reference number: A93984; MUID:83117859; PMID:6572010
A:Accession: A01283
A:Molecule type: mRNA

A:Residues: 1-436 <NAW>
A:Cross references: GB:J00010; GB:V00426; NID:9163256; PID:AAA30604.1; PID:g163257
C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of
xylophilic residue is present in the kininogen prior to the release of bradykinin.
C:Superfamily: kininogen; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; g
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-436/Product: LMW kininogen I #status predicted <MAT>
F:19-378/Product: LMW kininogen I heavy chain #status predicted <HC>
F:19-130/Domain: cystatin homology <CY1>
F:141-242/Domain: cystatin homology <CY2>
F:263-374/Domain: cystatin homology <CY3>
F:379-388/Product: lysyl-bradykinin (kallidin II) #status predicted <BDY>
F:380-388/Product: bradykinin (kallidin I) #status predicted <BDY>
F:389-396/Product: LMW kininogen I light chain #status experimental <LCB>
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:7-46, 82-93, 106-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/disulfide bond
F:47-87, 168, 169, 197-204/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:378-379/Cleavage site: Met-Lys (kininogen) #status predicted
F:388-389/Cleavage site: Arg-Ser (kininogen) #status predicted

Query Match 64.3%; Score 54; DB 1; Length 436;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NNATFYFKIDIVKKA 15
Db 292 HNHLYFYFKIDIVKKA 306

Query Match 64.3%; Score 54; DB 1; Length 436;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDIVKKA 15
Db 292 HDGAFYFKIDIVKKA 306

Query Match 64.3%; Score 54; DB 1; Length 436;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDIVKKA 15
Db 292 HDGAFYFKIDIVKKA 306

Query Match 66.7%; Score 56; DB 2; Length 430;
Best Local Similarity 73.3%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDIVKKA 15
Db 292 HNHLYFYFKIDIVKKA 306

A; Reference number: A91153; MUID: 86030270; PMID: 4054110 A; Content: annotation; bovine cleavage sites; bovine carbohydrate binding sites R; Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S. Seikagaku 56, 808, 1984	Db 33 NNLLFYSKYNNIKSR 48 RESULT 14 AH1213 TN916 ORF21 homolog lmo1112 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 C;Accession: AH1213 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Biolecz, J.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.; Science 294, 849-852, 2001 A; Authors: Kretf, J.; Kuhn, M.; Kunst, F.; Kurakpat, G.; Madueno, E.; Maltournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A; Title: Comparative genomics of <i>Listeria</i> species. A; Reference number: AB1077; MUID: 21537279; PMID: 11679669 A; Accession: AH1213 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-466 <GLA> A; Cross-references: GB:NC_000210; PIDN: CAC99190.1; PMID: g16410514; GSDB: GN00177 A; Experimental source: strain EGD-e C; Genetics: A; Gene: lmo1112
A; Title: Disulfide bonds in bovine HMW kininogens. A; Content: annotation; disulfide bonds A; Note: article in Japanese	Query Match 51.2%; Score 43; DB 2; Length 466; Best Local Similarity 60.0%; Pred. No. 22; Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0; C; Genetics: A; Gene: lmo1112
C; Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the HMW kininogen light chain is impo C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, 1 xyproline residue is present in kininogen prior to the release of bradykinin. C; Superfamily: kininogen; cystatin homology C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl F: 19-18/Domain: signal sequence #status predicted <SIG> F: 19-621/Product: HMW prokininogen I #status predicted <MAT> F: 19-379/Product: HMW kininogen I heavy chain #status experimental <HCH> F: 141-252/Domain: cystatin homology <CY1> F: 263-374/Domain: cystatin homology <CY2> F: 379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY> F: 380-388/Product: bradykinin (kallidin I) #status experimental <BDY> F: 389-621/Product: HMW kininogen I light chain #status experimental <LCH> F: 19/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F: 27, 591, 82-93, 106-125, 141-144, 205-217, 228-247, 263-266, 327-339, 350-369/disulfide bonds: F: 87, 168, 169, 204/Binding site: carbohydrate (Asn) (covalent) #status experimental 1 F: 136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental 1 F: 197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental 1 F: 318-379/Cleavage site: Met-Lys (kallikrein) #status experimental 1 F: 382/Modified site: 4-hydroxyproline (Pro) #status predicted F: 388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental 1 F: 399, 400, 520, 524, 536, 548, 553, 570/Binding site: carbohydrate (Thr) (covalent) #status ex F: 498-499/Cleavage site: Arg-Thr (kallikrein) #status experimental 1	RESULT 15 B84711 hypothetical protein At2g37310 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 C;Accession: B84791 R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 A; Title: Sequence and analysis of chromosome 2 of the plant <i>Arabidopsis thaliana</i> . A; Reference number: A84420; MUID: 20083487; PMID: 10617197 A; Accession: B84791 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-657 <STO> A; Cross-references: GB:AE002093; PIDN: AAC98051.1; GSDB: GN00139 C; Genetics: A; Gene: At2g37310 A; Map position: 2 C; Superfamily: Arabidopsis thaliana hypothetical protein T8H10.30
QY 1 NNATYEFKIDNVKK 15 Db 292 HDGAYFEKIDTVKRA 306	Query Match 64.3%; Score 54; DB 1; Length 621; Best Local Similarity 66.7%; Pred. No. 0.42; Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
RESULT 13 B97948 hypothetical protein ABC-NBD-truncation [imported] - Streptococcus pneumoniae (strain R6 C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 C;Accession: B97948 R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczaik, L.; Burgett, S.; Dehoff, B.S.; Fe e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M e, J. Bacteriol. 183, 5709-5717, 2001 A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A; Title: Genome of the Bacterium <i>Streptococcus pneumoniae</i> Strain R6. A; Reference number: A97872; MUID: 21429245; PMID: 11544234 A; Accession: B97948 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-217 <KUR> A; Cross-references: GB:AE007317; PIDN: AAK99414.1; PMID: g15458193; GSDB: GN00174 A; Gene: ABC-NBD-truncation	
QY 1 NNATYEFKIDNVKKAR 16 : :	Query Match 51.2%; Score 43; DB 2; Length 217; Best Local Similarity 50.0%; Pred. No. 10; Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
	Db 175 TYTKCDNIESAR 187
	Search completed: March 13, 2003, 19:14:02 Job time : 19 secs

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Result No.	Score	Query	Match	Length	DB ID	Description
1	84	100.0	644	1	KNG_HUMAN	PO1042 homo sapien
2	67	79.8	639	1	KNG_RAT	PO8934 rattus norv
3	59	70.2	434	1	KNL2_BOVIN	PO1047 bos taurus
4	59	70.2	619	1	KNH2_BOVIN	PO1045 bos taurus
5	56	66.7	430	1	KNT1_RAT	PO1048 rattus norv
6	56	66.7	430	1	KNT2_RAT	PO8932 rattus norv
7	54	64.3	436	1	KNL1_BOVIN	PO1046 bos taurus
8	54	64.3	621	1	KNH1_BOVIN	PO1044 bos taurus
9	53	63.1	661	1	KNG_MOUSE	PO8677 mus musculus
10	41	48.8	208	1	LEUD_BUCDN	PO83073 buchnera ap
11	41	48.8	1066	1	NUC2_NEUCR	Q13137 neurospora
12	39	46.4	237	1	Y70_CAEPEL	Q14180 caenorhabdi
13	39	46.4	306	1	YDS4_SCOPD	Q14180 schizosacch
14	39	46.4	406	1	HEFLK_BUCAI	P57631 buchnera ap
15	38	45.2	224	1	KCY_DRREP4	Q99geg ureaplasma ap
16	38	45.2	297	1	YDC1_SCOPD	Q10422 schizosacch
17	38	45.2	312	1	TRUB_BUCAI	P57456 buchnera ap
18	38	45.2	316	1	UFDL_DROME	Q14180 drosophila
19	38	45.2	513	1	PPTL_YEAST	P53043 sacccharomyces
20	37	44.0	219	1	Y413_RICPR	Q99db9 rickettsia
21	37	44.0	256	1	PXBB_CANBO	Q93117 candida boi
22	37	44.0	316	1	VSH5_DICDI	P44326 dictyosteli
23	37	44.0	365	1	OMIA_ACTPL	Q2937 actinobacil
24	37	44.0	384	1	YXP2_YEAST	P03879 sacccharomyces
25	37	44.0	452	1	PLML_PLAFA	P38898 plasmidium
26	37	44.0	470	1	SYE2_RICPR	Q99ct8 rickettsia
27	37	44.0	516	1	YCB2_EUGGR	P30397 euglena gra
28	37	44.0	550	1	DBP2_SCOPD	P24782 schizosacch
29	37	44.0	738	1	ST11_YEAST	P23561 sacccharomyces
30	37	44.0	1816	1	KFB1_MOUSE	Q61755 mus musculus
31	36.5	43.5	403	1	YA24_MEWA	Q58430 methanococcus
32	36.5	43.5	514	1	GUDC_FUSOX	P62338 fusarium ox
33	36	42.9	80	1	BMP3_BOVIN	P22444 bos tauru

Scoring table: BLOSUM62
Gapop 10.0 , Gapext. 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
List first 45 summaries

Database : SwissProt_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
KNG_HUMAN STANDARD; PRY; 644 AA.
ID KNG_HUMAN STANDARD; PRY;
AC P01042; P01043;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kininogen Precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Bradykinin].
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).
RC TISSUE=liver;
RX MEDLINE=85234582; PubMed=2989293;
RA Takagaki Y., Kitamura N., Nakaniishi S.;
RA Cloning and sequence analysis of cDNAs for human high molecular weight prekininogens. Primary structures of two human prekininogens. J. Biol. Chem. 260:8601-8609(1985).
RN [2]
RP GENE STRUCTURE.
RX MEDLINE=85234583; PubMed=2989294;
RA Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakanishi S.;
RA Structural organization of the human kininogen gene and a model for its evolution. J. Biol. Chem. 260:8610-8617(1985).
RN [3]
RP SEQUENCE OF 1-401 FROM N.A.
RX MEDLINE=85122621; PubMed=6441591;
RA Ohkubo I., Kurachi K., Takasawa T., Shiokawa H., Saasaki M.;
RT Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen. Biochemistry 23:5691-5697(1984).
RN [4]
RP SEQUENCE OF 379-644.
RX MEDLINE=8603270; PubMed=4054110;
RA LotteSpeich F., Kellermann J., Henschien A., Foertsch B., Mueller-Esterl W.;
RA The amino acid sequence of the light chain of human high-molecular-mass kininogen.;
RT Its identity with low molecular weight kininogen. Eur. J. Biochem. 152:307-314(1985).
RN [5]
RP SEQUENCE OF 381-389.
RX MEDLINE=90255622; PubMed=4952632;
RA Euglena gra;
RT "Structural features of Plasma kinins and kininogens.";
RL Proc. Natl. Acad. Sci. USA 85:1030-1034(1988).

[6]
RP DISULFIDE BONDS.
RA Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
"Disulfide bonds in bovine HMW kininogens.";
RT

age 3

"Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor."; J. Biol. Chem. 260:12054-12059(1985).

[3] SEQUENCE OF 1-65 FROM N.A.
STRAIN=Buffalo;
C STRAIN=Buffalo;
X MEDLINE=87250580; PubMed=2439509;
X Fung W.-P.; Schreiber G.;
A "Structure and expression of the genes for major acute phase alpha 1-
T protein (thielostatin) and kininogen in the rat.";
T J. Biol. Chem. 262:9298-9308(1987).

[4] SEQUENCE OF 1-41 FROM N.A.
STRAIN=Lister; TISSUE=Liver;
P MEDLINE=8713465; PubMed=3818598;
X Kageyama R.; Kitamura N.; Ohkubo H.; Nakanishi S.;
A "Differing utilization of homologous transcription initiation sites
of rat K and T kininogen genes under inflammation condition.";
T J. Biol. Chem. 262:2345-2351(1987).

[5] FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN AND PLASMIN-
INDUCED AGGREGATION OF THROMBOBLASTS; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) Natriuretic AND
DIURETICS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS). (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION;
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
CLOTTING.
SUBCELLULAR LOCATION: Secreted.

- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
- TISSUE SPECIFICITY: PLASMA.
- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
- MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS; THE CLASSICAL HMW/LMW KININOGENS AND TWO ADDITIONAL LMW LIKE KININOGENS: T-I AND T-II.
- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.

C EMBL; R L29428; AAA1486_1; - .
 C EMBL; R M11884; AAA1487_1; - .
 C EMBL; R M14369; AAA1484_1; - .
 C EMBL; R M14369; AAA1485_1; ALT_SEQ.
 C EMBL; R M16455; AAA1482_1; - .
 PIR; R A25486; A25486.
 PIR; R A28055; A28055.
 InterPro; R IPRO00010; Cystatin.
 InterPro; R IPRO02395; Kininogen.
 PRINTS; R PF0031; cystatin; 3.
 PRINTS; R PR0034; KININOGEN.
 SMART; R SM00043; CY; 3.
 PROSITE; R PS00287; CYSTATIN; 2.
 Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
 Bradysinin; Blood coagulation; Inflammatory response; Signal;
 SIGNAL; R Alternative splicing; Multigene family.
 SIGNAL; R 18

FT	CHAIN	19	639	KININOPEN.
FT	CHAIN	19	380	KININOPEN HEAVY CHAIN.
FT	PEPTIDE	381	389	BRADYKININ.
FT	CHAIN	390	639	KININOPEN LIGHT CHAIN.
FT	DOMAIN	19	136	CYSTATIN-LIKE 1.
FT	DOMAIN	137	258	CYSTATIN-LIKE 2.
FT	DOMAIN	259	380	CYSTATIN-LIKE 3.
FT	DOMAIN	439	514	HIS-RICH.
FT	DISULFID	28	609	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	63	94	BY SIMILARITY.
FT	DISULFID	107	126	BY SIMILARITY.
FT	DISULFID	142	145	BY SIMILARITY.
FT	DISULFID	206	218	BY SIMILARITY.
FT	DISULFID	229	248	BY SIMILARITY.
FT	DISULFID	264	667	BY SIMILARITY.
FT	DISULFID	328	340	BY SIMILARITY.
FT	DISULFID	351	370	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	127	127	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	529	529	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	402	433	WPSLTARLQRDPGRQEGDGHGMHAKQ -> RILIN (LMW).
FT	VARSPLIC	434	639	CEYKGRLKAGAGPAPERQAESTVTP (IN ISOFORM LMW).
FT	CONFLICT	61	61	MISSING (IN ISOFORM LMW).
SQ	SEQUENCE	639 AA;	70933 MW;	E -> K (IN REF. 2). D3172DF9EFF56A95 CRC64;
Query Match	Best Local Similarity	79.8%	score 67;	DB 1; Length 639;
Matches	13;	Conservative	86.7%;	Fred. No. 0.00095;
Qy	1	NNATFYFKIDNVKKAA	15	0; Mismatches 2; Indels 0; Gaps
Db	293	NNHTFYFKIDTVKKAA	307	
RESULT 3				
KNL2_BOVIN	ID	KNL2_BOVIN	STANDARD;	
AC	P01047;		PRT;	434 AA.
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Kininogen, LMW II precursor (Thiol proteinase inhibitor)	[Contains: Bradykinin].		
OS	Bos taurus (Bovine)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]	SEQUENCE FROM N.A.		
RX	MEDLINE=03117859;	PubMed=6572010;		
RX	MEDLINE=87137530;	PubMed=3546295;		
RA	Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;			
RT	"Primary structures of bovine liver low molecular weight kininogen precursors and their two mRNAs."			
RT	proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).			
RN	[2]	SEQUENCE OF 19-376.		
RX	SEQUENCE FROM N.A.			
RA	Sueyoshi T., Miyata T., Hashimoto N., Rato H., Hayashida H., Miyata T., Iwanaga S.;			
RT	"Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion."			
RT	J. Biol. Chem. 262:2768-2779 (1987).			
CC	-1- FUNCTION: (1) KININOPEN ARE INHIBITORS OF THIOL PROTEASES; (2) LMW-KININOPEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE ACTIVE PEPTIDE IN KININOPEN THAT IS RELEASED FROM LMW-KININOPEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS. (3A) INFLAMMATION IN SKIN			

DR EMBL; V01492; CAA24736_1; "major acute phase protein and alpha 1-cysteine proteinase inhibitor.";

DR EMBL; V01492; CAA24737_1; ALT_SEQ.

DR PIR; A01282; RGD012.

DR B29559; B29559.

DR HSSP; P01038; 1A90.

DR InterPro; IPR00010; Cystatin.

DR InterPro; IPR002395; Kininogen.

DR Pfam; PF00031; cystatin; 3.

DR PRINTS; PR00334; KININOGEN.

DR SMART; SM00043; CY_3.

DR PROSITE; PS00287; CYSTATIN; 2.

KW Glycoprotein; Plasma; Repeat; vasodilator; Alternative splicing; Signal;

KW Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;

KW Inflammatory response.

FT SIGNAL_1_18

FT CHAIN_19_619 KININOGEN, HMW II.

FT CHAIN_19_376 HEAVY CHAIN.

FT PEPTIDE_378_386 BRADYKININ.

FT DOMAIN_387_619 LIGHT CHAIN.

FT DOMAIN_19_135 CYSPATIN-LIKE 1.

FT DOMAIN_136_256 CYSPATIN-LIKE 2.

FT DOMAIN_257_376 CYSPATIN-LIKE 3.

FT MOD_RES_19_19 PYRROLIDONE CARBOXYLIC ACID.

FT CARBOHYD_87_87 N-LINKED (GLCNAC; . .).

FT CARBOHYD_136_136 O-LINKED (PARTIAL).

FT CARBOHYD_168_168 N-LINKED (GLCNAC; . .); OR 169.

FT CARBOHYD_197_197 N-LINKED (GLCNAC; . .) (PARTIAL).

FT CARBOHYD_204_204 N-LINKED (GLCNAC; . .).

FT CARBOHYD_280_280 N-LINKED (GLCNAC; . .).

FT CARBOHYD_400_400 O-LINKED.

FT DISULFID_27_589 INTERCHAIN.

FT DISULFID_82_93 DISULFID.

FT DISULFID_106_125 DISULFID.

FT DISULFID_141_144 DISULFID.

FT DISULFID_205_217 DISULFID.

FT DISULFID_228_247 DISULFID.

FT DISULFID_261_264 DISULFID.

FT DISULFID_325_337 DISULFID.

FT DISULFID_348_367 DISULFID.

FT VARIANT_398_401 VARIANT.

FT VARIANT_401_401 L -> V.

FT VARIANT_454_454 H -> K.

SQ SEQUENCE_619_AA_68710 MN; F04320A8EB0B0DA CRC64;

Query Match 1 NNATPFYFKIDNVKKA 15

Best Local Similarity 73.3%

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 5

ID KNT1_RAT STANDARD; PRT; 430 AA.

AC P01048; P04081.

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE T-kininogen I Precursor [Major acute phase protein] (Alpha-1-MAP)

DE (Thiostatin) [Contains: T-kinin].

GN MAP1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

MEDLINE=6600846; PubMed=2413018;

RA Furuto-Kato S.; Matsumoto A.; Kitamura N.; Nakaniishi S.;

RT "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with

RT major acute phase protein and alpha 1-cysteine proteinase inhibitor.";

RT J. Biol. Chem. 260:12054-12059(1985).

RL [2]

RN SEQUENCE OF 5-430 FROM N.A., AND PARTIAL SEQUENCE.

RP MEDLINE=86003266; PubMed=2413019;

RX MEDLINE=95127561; PubMed=2578992;

RA Cole T.; Inglis A.S.; Roxburgh C.M.; Howlett G.J.; Schreiber G.;

RA Anderson K.P.; Heath E.C.;

RT "The relationship between rat major acute phase protein and the kininogens.";

RT RN [3]

RN SEQUENCE OF 7-430 FROM N.A.

RX MEDLINE=95127561; PubMed=2578992;

RA Cole T.; Inglis A.S.; Roxburgh C.M.; Howlett G.J.; Schreiber G.;

RA "Major acute phase alpha 1-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";

RL FEBS Lett. 182:57-61(1985).

RN [4]

RP SEQUENCE OF 1-65 FROM N.A.

RX MEDLINE=87250580; PubMed=2439509;

RA Fung W.-P.; Schreiber G.;

RA "Structure and expression of the genes for major acute phase alpha 1-protein (thiostatin) and kininogen in the rat.";

RT Protein (thiostatin) and kininogen in the rat.;

RT RT

RL J. Biol. Chem. 262:9298-9308(1987).

CC -1: FUNCTION: KININOGENS ARE PLASMA GLYCOPROTEINS WITH A NUMBER OF FUNCTIONS: (1) AS PRECURSOR OF THE ACTIVE PEPTIDE BRADYKININ THEY EFFECT SMOOTH MUSCLE CONTRACTION, INDUCTION OF HYPOTENSION AND INCREASE OF VASCULAR PERMEABILITY. (2) THEY PLAY A ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII. (3) THEY ARE INHIBITOR OF THIOL PROTEASES.

CC -1: SUBCELLULAR LOCATION: Extracellular.

CC -1: TISSUE SPECIFICITY: PLASMA.

CC -1: INDUCTION: IN RESPONSE TO AN INFLAMMATORY STIMULANT. T-KININOGEN SYNTHESIS IS INDUCED AND THE PLASMA CONCENTRATION OF T-KININOGEN I IS RAISED.

CC -1: PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA KALLIKREIN.

CC -1: MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL HMW AND LMW KININOGENS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE, AND TWO ADDITIONAL LMW-LIKE DOMAINS.

CC -1: SIMILARITY: CONTAINS 3 CYSATIN-LIKE DOMAINS.

CC -1: CAUTION: IN ADDITION TO THE CONFLICTS DESCRIBED IN THE FEATURE TABLE, REF. 2, SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS: 257, 262, 268, 269, 295, 314, 315, 331, 332, AND 389. IN ALL THOSE POSITIONS THE ALTERNATE AMINO ACID IS THE ONE PRESENT IN T-II KININOGEN.

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CC EMBL; M11883; AAA1489_1; DR EMBL; M11661; AAA41570_1; DR EMBL; M16454; AAA41568_1; DR X02299; CAA26162_1; ALT_SEQ.

CC PIR; A01286; KGRTT1. DR PIR; A01285; KGRTM. DR PIR; A23897; A23897. DR PIR; A27115; A27115.

CC GlycoSuiteDB; P01048; DR InterPro; IPR00010; Cystatin. DR Pfam; PF000331; cystatin; 3. DR SMART; SM0042; Cr_3.

CC PROSITE; PS00287; CYSTATIN; 2. DR Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family; ! KW Thiol protease inhibitor; Bradykinin; Acute phase; Signal. FT SIGNAL_1_18

RESULT 7

KNN1_BOVIN STANDARD; PRN; 436 AA.

ID KNN1_BOVIN
AC P01046;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

Kininogen, LMW I precursor (Thiol protease inhibitor) [Contains:
DE Bradykinin]
OS Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
OX NCBI_TaxID=9913;

[1] RN SEQUENCE FROM N.A.; PubMed=83117859; PubMed=6572010;
RX MEDLINE=83117859; PubMed=6572010;
RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RT "Primary structures of bovine liver low molecular weight kininogen
precursors and their two mRNAs";
RT Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).

[2] RN SEQUENCE OF 19-378;
RX MEDLINE=87137530; PubMed=3546295;
RA Miyata T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RT Miyata T., Iwanaga S.;
RT "Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
chain portion.";
RT J. Biol. Chem. 262:2768-2779(1987).

-I- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC LMW KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
ACTIVE PEPTIDE KALLIDIN THAT IS RELEASED FROM LMW-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE ON SMOOTH
CC MUSCLE CONTRACTION. (3B) INDUCTION OF HYPOTENSION, (3C)
CC NATUREESIS AND DIURESIS (KIDNEY).
-I- SUBCELLULAR LOCATION: Extracellular.
CC -I- ALTERNATIVE PRODUCTS: 2 isoforms; LMW I (shown here) and HMW I
CC (AC P01046); are produced by alternative splicing.
CC -I- TISSUE SPECIFICITY: PLASMA.
CC -I- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
CC -I- MISCELLANEOUS: LMW KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT
CC INVOLVED IN BLOOD CLOTTING.
CC -I- SIMILARITY: CONTAINS 3 CYSSTIN-LIKE DOMAINS.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; V00426; CAA23709.1; [3]
DR PIR; A01283; KB0LL.
DR InterPro; IPR000010; Cystatin.
DR Pfam; PF00031; cystatin_3.
DR SMART; SM00043; cyt_3.
DR PROSITE; PS00287; CYSTATIN_2.
KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;
KW Thiol protease inhibitor; Bradykinin; Signal.

FT SIGNAL 1 18
FT CHAIN 19 436
FT CHAIN 19 378
FT PEPTIDE 380 388
FT CHAIN 389 436
FT DOMAIN 19 135
FT DOMAIN 136 257
FT DOMAIN 258 378
FT MOD_RES 19 19
FT CARBOHYD 87 87
FT CARBOHYD 136 136

FT CARBOHYD 168 168
FT CARBOHYD 197 197
FT CARBOHYD 204 204
FT DISULFID 27 406
FT DISULFID 82 93
FT DISULFID 106 125
FT DISULFID 141 144
FT DISULFID 205 217
FT DISULFID 228 247
FT DISULFID 263 266
FT DISULFID 327 339
FT DISULFID 350 369
FT CONFLICT 295 295
SQ SEQUENCE 436 AA; 48427 MW; F01F7EB6814BCE6C CRC64;

Query Match Score 54; DB 1; Length 436;
Best Local Similarity 64.3%; Score 54; DB 1; Length 436;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 8
KNN1_BOVIN STANDARD; PRN;
ID KNN1_BOVIN
AC P01044;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUN-2002 (Rel. 41, Last annotation update)
DE Kininogen, HMW I precursor (Thiol protease inhibitor) [Contains:
DE Bradykinin].
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN SEQUENCE FROM N.A.; PubMed=84014106; PubMed=6571699;
RX MEDLINE=84014106; PubMed=6571699;
RA Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RT "A single gene for bovine high molecular weight kininogens";
RT "Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the heavy
chain portion.";
RL Nature 305:545-549(1983).
RN SEQUENCE OF 19-378.
RX MEDLINE=87137530; PubMed=3546295;
RA Miyata T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Iwanaga S.;
RT "Studies on the structure of bovine kininogen: cleavages of disulfide
bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
RN SEQUENCE OF 378-498.
RX MEDLINE=70180420; PubMed=4986212;
RA Kato H., Nagasawa S., Suzuki T.;
RT RT
RN SEQUENCE OF 378-393.
RX MEDLINE=75170265; PubMed=1169237;
RA Han Y.N., Konya M., Iwanaga S., Suzuki T.;
RT RT
RN "Studies on the primary structure of bovine high-molecular-weight
kininogen. Amino acid sequence of a fragment (histidine-rich
peptide) released by plasma kallikrein. ";
J. Biochem. 77:55-68(1975).
RN [4]
RP SEQUENCE OF 458-498.
RX MEDLINE=75170265; PubMed=1169237;
RA Han Y.N., Konya M., Iwanaga S., Suzuki T.;
RT RT
RN "Studies on the primary structure of bovine kininogen: cleavages of disulfide
bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
CC -I- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC HMW KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND

PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW KININogen SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) Natriuresis and diuresis, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCTICEPtors (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION), INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION).

-1- SUBCELLULAR LOCATION: Extracellular.

-1- ALTERNATIVE PRODUCTS: 2 isoforms; HMW I (shown here) and LMW I (AC_P01046); are produced by alternative splicing.

-1- TISSUE SPECIFICITY: PLASMA.

CC -1- SIMILARITY: CONTAINS 3 Cystatin-like domains.

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DR EMBL; V01491; CAA24735..1; -

DR PIR; A01281; KGBOH1.

DR PIR; A29559; A29559.

DR InterPro; IPR000010; Cystatin.

DR InterPro; IPR002395; Kininogen.

DR Pfam; PF00031; cystatin; 3.

DR PRINTS; PR00334; KININogen.

DR SMART; SM00043; CY; 3.

DR PROSITE; PS00287; CYSTATIN; 2.

KW Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

KW Thiol protease inhibitor; Bradykinin; Blood coagulation;

KW Inflammatory response; Signal; 18 PROBABLE.

FT SIGNAL, 19 621 KININogen, HMW I.

FT CHAIN, 19 378 HEAVY CHAIN.

FT PEPTIDE, 380 388 BRADYKININ.

FT CHAIN, 389 621 LIGHT CHAIN.

FT DOMAIN, 19 135 CYSTATIN-LIKE 1.

FT DOMAIN, 136 257 CYSTATIN-LIKE 2.

FT DOMAIN, 258 378 CYSTATIN-LIKE 3.

FT MOD_RES, 19 19 PYRROLIDONE CARBOXYLIC ACID.

FT CARBOHYD, 87 87 N-LINKED (GLCNAC. . .).

FT CARBOHYD, 136 136 O-LINKED (PARTIAL).

FT CARBOHYD, 168 168 N-LINKED (GLCNAC. . .); OR 169.

FT CARBOHYD, 197 197 N-LINKED (GLCNAC. . .) (PARTIAL).

FT CARBOHYD, 204 204 N-LINKED (GLCNAC. . .).

FT DISULFID, 27 591 INTERCHAIN.

FT DISULFID, 82 93

FT DISULFID, 106 125

FT DISULFID, 141 144

FT DISULFID, 205 217

FT DISULFID, 228 247

FT DISULFID, 263 266

FT DISULFID, 327 339

FT DISULFID, 350 369

SQ SEQUENCE, 621 AA; 68890 MW; D16850BBFE3C55CD CRC64;

KNG_MOUSE STANDARD; PRT; 661 AA.

ID KNG_MOUSE ID 008677; 008676;

AC 008677; 008676;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Kininogen precursor [Contains: Bradykinin].

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.

OC OC

OX OX

RA RA

RP RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).

RC RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;

RT RT "Molecular cloning of cDNAs for mouse low- and high-molecular kininogen." Takanoh M., Kondooh J., Yamaya K., Okamoto H.;

RT Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

RL -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESES, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPtors (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS). (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELION-DERIVED RELAXING FACTOR ACTION); (5) LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD CLOTTING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -1- TISSUE SPECIFICITY: PLASMA.

CC -1- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.

CC -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.

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CC EMBL; D84435; BAA19743..1; -

DR EMBL; D84415; BAA19742..1; -

DR MGD; MGI:1097705; Kng.

DR InterPro; IPR000010; Cystatin.

DR InterPro; IPR002395; Kininogen.

DR Pfam; PF00031; cystatin; 3.

DR PRINTS; PR00334; Kininogen.

DR SMART; SM00043; CY; 3.

DR PROSITE; PS00287; CYSTATIN; 1.

KW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal; KW Alternative splicing

POTENTIAL.

FT SIGNAL, 18 KININOGEN.

FT CHAIN, 19 KININOGEN HEAVY CHAIN.

FT CHAIN, 19 379 KININOGEN LIGHT CHAIN.

FT CHAIN, 380 388 KININOGEN LIGHT CHAIN.

FT DOMAIN, 19 135 CYSTATIN-LIKE 1.

FT DOMAIN, 136 257 CYSTATIN-LIKE 2.

FT DOMAIN, 258 378 CYSTATIN-LIKE 3.

FT MOD_RES, 19 19 KININOGEN.

FT CARBOHYD, 87 87 KININOGEN.

FT CARBOHYD, 136 136 KININOGEN.

FT CARBOHYD, 168 168 KININOGEN.

FT CARBOHYD, 197 197 KININOGEN.

FT CARBOHYD, 204 204 KININOGEN.

FT DISULFID, 27 591 KININOGEN.

FT DISULFID, 82 93 KININOGEN.

FT DISULFID, 106 125 KININOGEN.

FT DISULFID, 141 144 KININOGEN.

FT DISULFID, 205 217 KININOGEN.

FT DISULFID, 228 247 KININOGEN.

FT DISULFID, 263 266 KININOGEN.

FT DISULFID, 327 339 KININOGEN.

FT DISULFID, 350 369 KININOGEN.

SQ SEQUENCE, 621 AA; 68890 MW; D16850BBFE3C55CD CRC64;

Query Match 64.3%; Score 54; DB 1; Length 621;

Best Local Similarity 66.7%; Pred. No. 0.14; Gaps 0;

Matches 10; Conservative 2; Mismatches 3; Indels 0;

FT SIGNAL, 18 KININOGEN.

FT CHAIN, 19 KININOGEN HEAVY CHAIN.

FT CHAIN, 19 379 KININOGEN LIGHT CHAIN.

FT CHAIN, 380 388 KININOGEN LIGHT CHAIN.

FT DOMAIN, 19 135 CYSTATIN-LIKE 1.

FT DOMAIN, 136 257 CYSTATIN-LIKE 2.

FT DOMAIN, 258 389 KININOGEN LIGHT CHAIN.

FT DOMAIN, 439 524 HIS-RICH.

FT DISULFID 28 631

RESULT 9

FT DISUFLID 83 94 BY SIMILARITY.
 FT DISUFLID 107 125 BY SIMILARITY.
 FT DISUFLID 141 144 BY SIMILARITY.
 FT DISUFLID 205 247 BY SIMILARITY.
 FT DISUFLID 228 247 BY SIMILARITY.
 FT DISUFLID 263 266 BY SIMILARITY.
 FT DISUFLID 327 339 BY SIMILARITY.
 FT DISUFLID 350 369 BY SIMILARITY.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VSPPLTAREDEERDAETEGPHTGHGWLEKQ 432 RLRRA
 CEYKGRLSKAGAEPAAPERQAESSQVKQ (IN ISOFORM
 LAW).
 FT VARSPLIC 433 661 MISSING (IN ISOFORM LMW).
 SQ SEQUENCE 661 AA; 73102 MW; 7744602586 CRC64;

Query Match 63.1%; Score 53; DB 1; Length 61;
 Best Local Similarity 66.7%; Pred. No. 0.22;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDNVKK 15
 | : ||:||| |||||
 Db 292 NDHPFYKIDTVKKA 306

RESDT 10
 LEUD_BUCDN STANDARD; PRT; 208 AA.
 ID LEUD_BUCDN STANDARD; PRT; 208 AA.
 AC 085073; 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
 DE (Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI).
 LEUD OS Buchnera aphidicola (subsp. Diuraphis noxia).
 OC Plasmid pLeu-nm (pBDn1).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118101;

RN [1] SEQDEFNCE FROM N.A.
 RA Baumann L., Baumann P., Moran M.A., Sandstrom J., Thao M.L.;
 RT "Genetic characterization of plasmids containing genes encoding
 enzymes of leucine biosynthesis in endosymbionts (Buchnera) of two
 related aphid species." Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: 2'-ISOPROPYLALATE = 2'-ISOPROPYLALATE +
 H(2)O (ALSO CATALYSIS: 2'-ISOPROPYLALATE + H(2)O = 3-HYDROXY-
 4'-METHYL-3-CARBOXYPENTANONE).
 CC -1- PATHWAY: Leucine biosynthesis; second step.
 CC -1- SUBUNIT: CONSISTS OF TWO DIFFERENT SUBUNITS: LEUD AND LEUD.

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 or send an email to license@lsb-sib.ch).

DR EMBL; AF041837; AAD12603 1; -
 DR InterPro; IPR00573; Aconitase_C.
 DR InterPro; IPR004431; LeuID.
 DR Pfam; PF00694; Aconitase_C; 1.
 DR TIGRFAMS; TIGR0117; LeuID; 1.
 KW Leucine biosynthesis; Lyase; Plasmid.

SQ SEQUENCE 208 AA; 24266 MW; E40CD8A63F0396B5 CRC64;

Query Match 48.8%; Score 41; DB 1; Length 208;
 Best Local Similarity 42.9%; Pred. No. 7.1;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0; Gaps 0;

RESDT 11
 NUC2_NEUCR STANDARD; PRT; 1066 AA.
 ID NUC2_NEUCR STANDARD; PRT; 1066 AA.
 AC Q01317;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

Db 155 NKATFFKLFDEERR 168

RESDT 12
 YS76_CAEEL STANDARD; PRT; 237 AA.
 ID YS76_CAEEL STANDARD; PRT; 237 AA.
 AC Q09619;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

Qy 1 NNATFYFKID 10
 | : ||:|||
 Db 63 NKATFFQFID 72

Query Match 48.8%; Score 41; DB 1; Length 1066;
 Best Local Similarity 70.0%; Pred. No. 38;
 Matches 7; Conservative 70.0%; Mismatches 1; Indels 0; Gaps 0;

DE Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Armstrong S.L., Forsburg S.L.,
 GN Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 OS Caenorhabditis elegans.
 RA Sipakowski G.V., Ussey D., Barrett B.G., Nurse P.;
 OC Rhabditidae; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 NCBI_TAXID=6239;
 OX Rhabditidae; Peleoderaiae; Caenorhabditida.
 RN [1]

SEQUENCE FROM N.A.
 STRAIN=Bristol N2;
 RP RC Hypothetical protein (MAR-1995) to the EMBL/GenBank/DBJ/ databases.
 RL CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
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 CC -----
 DR EMBL; Z98530; CAB11051; 1;
 DR InterPro; IPR02799; Imp4.
 DR Pfam; PF01945; Imp4; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 306 AA; 35835 MW; 2029FBB2358BC01E CRC64;

Query Match 46-48; Score 39; DB 1; Length 306;
 Best Local Similarity 37.5%; Pred. No. 23;
 Sequence 237 AA; 27303 MW; 3C54CD6CP38BEA269 CRC64;

Query Match 46-48; Score 39; DB 1; Length 237;
 Best Local Similarity 54.5%; Pred. No. 18;
 Sequence 237 AA; 27303 MW; 3C54CD6CP38BEA269 CRC64;

Query 1 NNATFYFKIDNVKKAR 16
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Sequence 237 AA; 27303 MW; 3C54CD6CP38BEA269 CRC64;

RESULT 14
 HFLK_BUCAI STANDARD PRT; 406 AA.
 ID HFLK_BUCAI AC P57631;
 DE 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE HFLK protein.
 GN Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OS Buchnera sp.; Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OC NCBI_TAXID=118099;
 RN [1]
 RP Sequence from N.A.
 RC STRAIN=Tokyo 1998;
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 RT Buchnera sp. APS";
 RL Nature 407:81-86(2000);
 CC 1- FUNCTION: HFLC AND HFLK COULD ENCODE OR REGULATE A PROTEASE (BY
 SIMILARITY).
 CC 1- SUBUNIT: HFLC AND HFLK MAY INTERACT TO FORM A MULTIMERIC COMPLEX
 (BY SIMILARITY).
 CC 1- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY. HFLK SUBFAMILY.

Query Match 46-48; Score 39; DB 1; Length 306;
 Best Local Similarity 37.5%; Pred. No. 23;
 Sequence 237 AA; 27303 MW; 3C54CD6CP38BEA269 CRC64;

Query 1 NNATFYFKIDNVKKAR 16
 Best Local Similarity 54.5%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Sequence 237 AA; 27303 MW; 3C54CD6CP38BEA269 CRC64;

RESULT 13
 YDS4_SCPO STANDARD PRT; 306 AA.
 AC O14180; 36, Created
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C4F8.04 in chromosome I.
 GN SPA4F8.04.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Schizosaccharomyces pombe; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetidae;
 OX NCBI_TAXID=4896;
 RN [1]
 RP Sequence from N.A.
 RC STRAIN=972;
 RX MEDLINE=2168401; PubMed=11959360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 SGouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howard S., Huckle E.J., Hunt S., Jagels R.,
 RA James K., Jones L., Jones M., Leather S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., niblett D., Odell C.,
 RA Oliver R., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Gromponez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Burst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

SQ SEQUENCE 406 AA; 46928 MW; 70BA5DD72E537DB2 CRC64;
 Query Match 46.4%; Score 39; DB 1; Length 406;
 Best Local Similarity 54.5%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 NNATFYFKIDN 11
 Db 334 NNPMEFFSLLN 344

RESULT 15
 KCY_UREPA
 ID KCY_UREPA
 AC Q9PQ99;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytidylylate kinase (EC 2.7.4.14) (CK) (Cytidine monophosphate kinase)
 DE (CMP kinase).
 DE CMK OR UU342.
 GN OS ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
 OX NCBI_TAXID=13421;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Serovar 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lettkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
 RA Cassell G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 urealyticum."
 RL Nature 407:757-762(2000).
 CC -1 - CATALYTIC ACTIVITY: ATP + (d)CDP = ADP + (d)CDP.
 CC -1 - SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1 - SIMILARITY: BELONGS TO THE CYTIDYLATE KINASE FAMILY. SUBFAMILY 1.

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CC EMBL: AE002131; AAF30751; -.
 DR HSSP: P23863; ICKE.
 DR InterPro: IPR003136; Cytidylylate_kin.
 DR Pfam: PF0224; Cytidylylate_kin; 1.
 DR TIGR00017; cmk:1.
 KW Transferase; Kinase; ATP-binding; Complete proteome.
 NP_BIND FT 11 19 ATP (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 25618 MW; AEEE7DFF423DADFF CRC64;

Query Match 45.3%; Score 38; DB 1; Length 224;

Best Local Similarity 66.7%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NATFYFKIDNK 13
 ||| | |||||
 Db 66 NANFIGNDWK 77

Search completed: March 13, 2003, 19:13:26
 Job time : 12 secs

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GenCore version 5.1.4_D5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:27 ; Search time 33.3333 Seconds
(without alignments)
98.903 Million cell updates/sec

Title: US-09-461-061a-10
Perfect score: 84
Sequence: 1 NNATYEFKIDNVKKAR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_invertebrate;*
- 5: sp_mammal;*
- 6: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriopl;*
- 17: sp_archeap;*

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	56	66.7	P70517	P70517 ratius norv
2	56	66.7	Q63581	Q63581 ratius norv
3	53	63.1	Q91XK5	Q91XK5 mus musculu
4	53.6	43.2	Q8T2A3	Q8T2A3 dictyostelli
5	44	52.4	Q9KTB1	Q9KTB1 porphyromon
6	43	51.2	Q8Y807	Q8Y807 listeria mo
7	42	50.0	Q8WL12	Q8WL12 chlorogonium
8	42	50.0	QBWU11	QBWU11 ankistrodes
9	42	50.0	Q9ZUT5	Q9ZUT5 rabidopsis
10	41.5	49.4	Q29037	Q29037 archaeoglob
11	41.5	49.4	Q95P10	Q95P10 dictyosteli
12	41	48.8	Q8XMH6	Q8XMH6 clostridium
13	41	48.8	Q8R468	Q8R468 fusobacteri
14	41	48.8	Q9V0Z1	Q9V0Z1 pyrococcus
15	41	48.8	Q94IR2	Q94IR2 phaeococcus
16	41	48.8	Q9ENR4	Q9ENR4 ammacta moo

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	56	66.7	P70517	P70517 ratius norv
2	56	66.7	Q63581	Q63581 ratius norv
3	53	63.1	Q91XK5	Q91XK5 mus musculu
4	53.6	43.2	Q8T2A3	Q8T2A3 dictyostelli
5	44	52.4	Q9KTB1	Q9KTB1 porphyromon
6	43	51.2	Q8Y807	Q8Y807 listeria mo
7	42	50.0	Q8WL12	Q8WL12 chlorogonium
8	42	50.0	QBWU11	QBWU11 ankistrodes
9	42	50.0	Q9ZUT5	Q9ZUT5 rabidopsis
10	41.5	49.4	Q29037	Q29037 archaeoglob
11	41.5	49.4	Q95P10	Q95P10 dictyosteli
12	41	48.8	Q8XMH6	Q8XMH6 clostridium
13	41	48.8	Q8R468	Q8R468 fusobacteri
14	41	48.8	Q9V0Z1	Q9V0Z1 pyrococcus
15	41	48.8	Q94IR2	Q94IR2 phaeococcus
16	41	48.8	Q9ENR4	Q9ENR4 ammacta moo

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
P70517 PRELIMINARY;
ID P70517; AC P70517; DT 01-FEB-1997 (TREMBL); 02, Created)
SP organelle;* DE Major acute phase alpha(1)-protein (Rat).
OS Rattus norvegicus (Rat). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
RN [11] RA SEQUENCE FROM N.A.
RN [12] RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN [1] RP SEQUENCE FROM N.A.
RX MEDLINE=85149311; PubMed=2579644;
RA Cole T., Inglis A.S., Nagashima M., Schreiber G.; RT "Major acute phase alphal-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";
RL Biochem. Biophys. Res. Commun. 136:719-724 (1985).
RN [13] RP SEQUENCE FROM N.A.
RX MEDLINE=85127561; PubMed=2578992;
RA Cole T., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.; RT "Major acute phase alphal-protein of the rat is homologous to bovine kininogen and contains the sequence for bradykinin: its synthesis is regulated at the mRNA level.";
RL FEBS Lett. 182:57-61 (1985).
DR EMBL; K02811; AAA15691.; DR InterPro; IPR00010; Cystatin.
DR Pfam; PF00031; cystatin; 3. DR SMART; SM0043; CY; 3.
DR PROSITE; PS00287; Cystatin; 2. DR Signal.
FT NON_TER <1 1 POTENTIAL.
FT SIGNAL <1 1 POTENTIAL.

RESULT 2
 ID Q63581; PRELIMINARY; PRT; 430 AA.
 AC Q63581;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Rat T-kininogen (T-KG).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP .SEQUENCE FROM N.A.
 RX MEDLINE=9034172; PubMed=2805908;
 RA Andersson K.P., Croyle M.L., Lingrel J.B.;
 RT "Primary structure of a gene encoding rat T-kininogen.";
 Gene 8:119-128(1985).
 DR M29050; AAA42251..
 EMBL; M29083; AAA42251..1; JOINED.
 DR EMBL; M29084; AAA42251..1; JOINED.
 DR EMBL; M29091; AAA42251..1; JOINED.
 DR EMBL; M29085; AAA42251..1; JOINED.
 DR EMBL; M29086; AAA42251..1; JOINED.
 DR EMBL; M29087; AAA42251..1; JOINED.
 DR EMBL; M29088; AAA42251..1; JOINED.
 DR EMBL; M29089; AAA42251..1; JOINED.
 DR InterPro; IPR00010; Cystatin.
 DR Pfam; PF00031; cystatin_3.
 DR SMART; SM0043; Cy_3.
 DR PROSITE; PS00267; CYSTATIN_2.
 SQ SEQUENCE 430 AA; 47618 MW; 45508DEF4BDC978C CRC64;
 Query Match 66.7%; score 56; DB 11; Length 430;
 Best Local Similarity 73.3%; Pred. No. 0.55%; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
 ID Q91XK5; PRELIMINARY; PRT; 432 AA.
 AC Q91XK5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Adult female Placenta cDNA, RIKEN full-length enriched library,
 DE clone:160002701, full insert sequence (Kininogen).
 GN KNG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RA Submitter (JUL-2000) to the EMBL/GenBank/DBJ databases.

RESULT 4
 ID Q8TA3 PRELIMINARY; PRT; 806 AA.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RA Submitter (JUL-2000) to the EMBL/GenBank/DBJ databases.

RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakawa T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kohama Y.,
 RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
 RA Nishii K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
 RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
 RA Shiba K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
 RA Suzuki H., Tagami M., Takahashi F., Tanaka T., Tejima Y.,
 RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshiino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RX MEDLINE=24085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RX MEDLINE=93279233; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Hayatsu N., Sugahara Y., Shabata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP .SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PLACENTA;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shiba K., Ichoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishii Y., Nakamura T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Hezama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujikawa S., Inoue K., Togawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kura A., Hayashizaki Y.;
 RT "RIKEN integrated sequencing system (RISA) system-384 format
 sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP .SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK00547; BAB2415..1;
 DR EMBL; BC018158; AA18158..1;
 DR MGD; MG1:1097705; KnG.
 DR InterPro; IPR00010; Cystatin.
 DR Pfam; PF00031; cystatin_3.
 DR PROSITE; PS00287; CYSTATIN; UNKNOWN 1.
 SQ SEQUENCE 432 AA; 47838 MW; 9854EDAS284A16B CRC64;

Query Match 63.1%; Score 53; DB 11; Length 432;
 Best Local Similarity 66.7%; Pred. No. 1.7%;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKA 15
 DB 292 NHHTFYFKIDNVKKA 306

AC Q8T2A3; DT 01-JUN-2002 (TREMBLrel. 21, Created) DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Hypothetical 96.2 kDa protein. OS Dictyostelium discoideum (Slime mold). OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium. NCBI_TaxID=44689; OX [1] RN SEQUENCE FROM N.A. RP STRAIN=N-AX4; RC Sequence from N.A. RA Gleckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Rosenthal A., Noegel A.A.; RT "Sequence and Analysis of Chromosome 2 of Dictyostelium." Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. EMBL: AC115678; AAI92605.1; -. DR Hypothetical protein. KW SEQUENCE 806 AA; 96216 MW; 2D9BDB77A5BAD1F6 CRC64;

Query Match 53.6%; Score 45; DB 5; Length 806; Best Local Similarity 57.1%; Pred. No. 60; Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0; SQ

Qy 1 NNATPFKIDNVKK 14 Db 146 NNYPYFTLDETKK 159

RESULT 5 ID Q9KIB1 PRELIMINARY; PRT; 867 AA.

AC Q9KIB1; DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE Hypothetical tonB-linkerd outer membrane receptor PG47. OS Porphyromonas gingivalis (Bacteroides gingivalis). OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaeae; NCBI_TaxID=837; OX [1] RN SEQUENCE FROM N.A. RP STRAIN=N-W10; RC Ross B., Barr I., Patterson M., Agius C., Rothel L., Margetts M., Hocking D., Webb E.; RT "P. gingivalis Polypeptides and nucleic acids." Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases. RL [2] RN SEQUENCE FROM N.A. RP STRAIN=W450; RC Receptor; KW SEQUENCE 867 AA; 95231 MW; FAB4842E821C4E8E CRC64;

Query Match 52.4%; Score 44; DB 2; Length 867; Best Local Similarity 53.3%; Pred. No. 93; Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0; SQ

Qy 2 NATPFKIDNVKK 16 Db 816 STTFVNMDNADKR 830

RESULT 6 Q8Y807 ID Q8Y807 PRELIMINARY; PRT; 466 AA.

AC NCBI_TaxID=1639; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=EGD-E / SEROVAR 1/2A; MEDLINE=2153779; PubMed=11679669; RX Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Biocker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Darvillat A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeot O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garilio P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaeberl U., Krefl J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitouram A., Mata Vicente J., Ng B., Nedjari H., Nordiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.; RT "Comparative genomics of Listeria species." RL Science 294:849-852(2001); EMBL: AL591977; CAC9190.1; -. DR ListList; LN001112; -. DR InterPro; IPR002543; FTsK_SpoIIIE. DR Pfam; PF01580; FtSK_SpoIIIE; 1. KW Hypothetical protein; Complete proteome. SQ SEQUENCE 466 AA; 53666 MW; ED1937AD8335336F3 CRC64;

RESULT 7 Q8WLI2 PRELIMINARY; PRT; 229 AA.

ID Q8WLI2; AC Q8WLI2; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update) DE Chloroplast large-subunit ribosomal RNA (rrnL), site-specific DNA endonuclease I-Cell gene. DE endonuclease I-Cell gene. OS Chloroplast. OG Chloroplast. OC Eukaryota; Viridiplantae; Chlorophyta; Volvocales; OC Haematoococcaceae; Chlorogonium. OX NCBI_TaxID=52029; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=27331047; PubMed=9185572; RA Turnel M., Otis C., Cote V., Lemieux C.; RT "Evolutionarily conserved and functionally important residues in the I-Cell homing endonuclease." RL Nucleic Acids Res. 25:2610-2619 (1997). DR L42860; AAL34336.1; -. DR InterPro; IPR001982; Endonuc_LAG/HNH. DR Pfam; PF00961; LAGLIDADG_1. KW Chloroplast. SQ SEQUENCE 229 AA; 26622 MW; 5C7EF3DQDC27521E CRC64;

Query Match 50.0%; Score 42; DB 8; Length 229; Best Local Similarity 72.7%; Pred. No. 54; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1 NNATFYFKIDN 11 :	PRELIMINARY;	PRT;	244 AA.
Db	126 SNATMVKIDN 136			
RESULT 8				
Q8WL11	ID Q8WL11; PRELIMINARY; AC Q8WL11; SEQUENCE FROM N.A.; DT 01-MAR-2002 (TREMBLrel. 20, Created) DT 01-JUN-2002 (TREMBLrel. 20, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
	Chloroplast large-subunit ribosomal RNA (rrnl), site-specific DNA endonuclease I-AstI gene.			
	DE Ankistrodesmus stipitatus.			
	OG Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae; OC Ankistrodesmus. OX NCBI_TaxID=3109;			
	RN [1]			
	RP SEQUENCE FROM N.A.; PubMed=9185572; RX MEDLINE=91331047; Last sequence update)			
	RA Turnel M., Otis C., Cote V., Lemieux C., RT Evolutionarily conserved and functionally important residues in the RT I-Cell homing endonuclease."; RT Nucleic Acids Res. 25: 2610-2619(1997). RL EMBL; LA2384; AAL3430.1; -. DR InterPro; IPR001982; Endonuc_LAG/HNN. DR Pfam; PF00961; LAGLDADG_1; 1. KW Chloroplast.			
	RN [1]			
	SQ SEQUENCE 244 AA.; BA53E451E11FCCF2 CRC64;			
	Query Match Score 42%; DB 8; Length 244; Best Local Similarity 72.7%; Fred. No. 57; Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;			
Qy	1 NNATFYFKIDN 11 :	PRELIMINARY;	PRT;	657 AA.
Db	130 SNATMVKIDN 140			
RESULT 9				
Q9ZUT5	ID Q9ZUT5; PRELIMINARY; AC Q9ZUT5; SEQUENCE FROM N.A.; DT 01-MAY-1999 (TREMBLrel. 10, Created) DT 01-JUN-2002 (TREMBLrel. 10, Last sequence update) DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
	GN AT2637310. protein.			
	OC Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
	OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
	OX NCBI_TaxID=3702;			
	RN [1]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20083487; PubMed=10617197;			
	RX Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 10				
O29037	ID O29037; PRELIMINARY; AC O29037; PRT;	469 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;			
	RX MEDLINE=98049343; Published 9/30/94 75;			
	RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.B., Ketchum K.A., Dodson R.J., Gwynn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loitus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowm C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;			
	RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; RL Nature 390:364-370(1997).			
	RT "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; RL Nature 390:364-370(1997).			
	RN [1]			
	SQ SEQUENCE 469 AA.; 51663 MW; 3BDA6AFB179BB43 CRC64;			
	Query Match Score 41.5%; DB 17; Length 469; Best Local Similarity 83.3%; Pred. No. 1.3e+02; Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
Qy	2 NATFYFKIDN 13 	PRELIMINARY;	PRT;	1548 AA.
Db	335 NATFYKL-NVK 345			
RESULT 11				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20010119; Created DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 12				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 13				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 14				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 15				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 16				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 17				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 18				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 19				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 20				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 21				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 22				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 23				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 24				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA; MEDLINE=20020121; Last annotation update)			
	RA Buel C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
	RN [2]			
	RP SEQUENCE FROM N.A.; RC STRAIN=CV; COLUMBIA;			
	RA Lin X., Raul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D., Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., vanAken S.E., DnaAy L., Tallon J.E., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaven G.P., Preuss D., Nieman W.C., White O., Elsen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana"; Nature 402:761-768(1999).			
RESULT 25				
O95PIO	ID O95PIO; PRELIMINARY; AC O95PIO; PRT;	1548 AA.		

RN	[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RC	STRAIN=AX-;	
RA	Anjard C.; Loomis W.F.;	
RT	"The histidine kinases of Dictyostelium.";	
RL	(In) Inouye M., Dutta R. (eds.);	
RT	Histidine Kinases in Signal Transduction, pp.1-1, Academic Press,	
RL	San Diego (2001).	
[2]		
RN	SEQUENCE FROM N.A.	
RP	STRAIN=AX-;	
RC	Anjard C.; Loomis W.F.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	
DR	EMBL; AF32368; AAK54087.2; -.	
KW	Kinase	
SQ	SEQUENCE 1548 AA; 175972 MW; A65783B3AD984596 CRC64;	
Query Match	49.4%; Score 41.5; DB 5; Length 1548;	
Best Local Similarity	60.0%; Pred. No. 4.1e+02;	
Matches	9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;	
Qy	1 NNATYFYF-KIDNVKK 14	
Db	5 NNSQYFYHKDDKIKK 19	
RESULT 12		
Q8XMH6	PRELIMINARY;	PRT; 154 AA.
ID	Q8XMH6;	
AC	Q8XMH6;	
DT	01-MAR-2002 (TREMBLrel. 20, Created)	
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Hypothetical protein CPE0113.	
GN	CPE0113.	
OS	Bacterium perfringens.	
OC	Bacteria; Firmicutes; Clostridia; Clostridium group; Clostridia;	
OC	Clostridia; Clostridiaceae; Clostridium.	
OX	NCBI_TaxID=1502;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=13 / TYPE A;	
RX	PubMed=11792842;	
RA	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,	
RA	Shiba T., Ogasawara N., Hattori M., Kuwara S., Hayashi H.;	
RT	"Complete genome sequence of Clostridium perfringens, an anaerobic	
RT	"flesh eater".	
RT	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).	
RL	EMBL; AP0031187; BAB00419.1; -.	
DR	Hypothetical protein; Complete proteome; 97C25B68403A4B5B CRC64;	
KW	SEQUENCE 154 AA; 179711 MW;	
Query Match	48.8%; Score 41; DB 16; Length 154;	
Best Local Similarity	53.8%; Pred. No. 53;	
Matches	7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Qy	4 TTYFYKIDNVKK 16	
Db	128 TLYFLDYLKKK 140	
RESULT 13		
Q8RH68	PRELIMINARY;	PRT; 417 AA.
ID	Q8RH68;	
AC	Q8RH68;	
DT	01-JUN-2002 (TREMBLrel. 21, Created)	
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Rod shape-determining protein rodA.	
GN	FN0042.	
OS	Fusobacterium nucleatum (subsp. nucleatum).	
OC	Bacteria; Fusobacteria; Fusobacterium.	
NCBI_TaxID=768356;		
OX		
RESULT 14		
Q9V0Z1	PRELIMINARY;	PRT; 454 AA.
ID	Q9V0Z1;	
AC	Q9V0Z1;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Hypothetical protein PAB1940.	
GN	PAB1940.	
OS	Pyrococcus abyssi.	
OC	Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;	
OC	Pyrococcus.	
NCBI_TaxID=29492;		
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ORSAY;	
RA	Heilig R.;	
RT	"Pyrococcus abyssi genome sequence: insights into archaeal chromosome	
RT	structure and evolution";	
RT	Submitted (JUL-1999) to the EMBL/GenBank/ DDBJ databases.	
RL	InterPro: IPR00357; HEAT_REPEAT.	
DR	PROSITE: PS50077; HEAT_REPEAT_1.	
KW	Hypothetical protein; Complete proteome.	
SEQUENCE 454 AA; 52171 MW;		
Query Match	48.8%; Score 41; DB 17; Length 454;	
Best Local Similarity	57.1%; Pred. No. 1.5e+02;	
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	
Qy	1 NNATYFYKIDNVKK 14	
Db	316 SNATSYKIDDAK 329	
RESULT 15		
Q94IR2	PRELIMINARY;	PRT; 543 AA.
ID	Q94IR2;	
AC	Q94IR2;	
DT	01-DEC-2001 (TREMBLrel. 19, Created)	
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Carotenoid 9,10-9',10', cleavage dioxygenase.	
CCD1.		
GN	Phaseolus vulgaris (Kidney bean) (French bean).	
OS	Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicots; Rosidae; Phaseolidae.	
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Phaseoloidae.	
OC		

OX NCBI_TaxID=38885;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz S.H., Qin X., Zeevaart J.A.D.;
RT "Characterization of a Novel Carotenoid Cleavage Dioxygenase from
Plants";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AY029525; AAK38744; 1;
DR InterPro: IPR04234; RPB65;
DR Pfam: PF03055; RPB65; 1.
KW Dioxygenase.
SQ SEQUENCE 543 AA; 61100 MW; F22C9883A05325F7 CRC64;
Query Match 48.8%; Score 41; DB 10; Length 543;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 2 NATFYFKIDNVKKAR 16
| | | : |||
Db 298 NKTLIFSPDSTKKAR 312

Search completed: March 13, 2003, 19:13:05
Job time : 36.3333 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:07 ; Search time' 21 Seconds

(without alignments)
50.762 Million cell updates/secTitle: US-09-461-061A-1
Perfect score: 45

Sequence: 1 NNATYFK 8

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1981.DAT;*
- 3: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1982.DAT;*
- 4: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1983.DAT;*
- 5: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1984.DAT;*
- 6: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1985.DAT;*
- 7: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1986.DAT;*
- 8: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1987.DAT;*
- 9: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1988.DAT;*
- 10: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1989.DAT;*
- 11: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1990.DAT;*
- 12: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1991.DAT;*
- 13: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1992.DAT;*
- 14: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1993.DAT;*
- 15: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1994.DAT;*
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- 17: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1996.DAT;*
- 18: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1997.DAT;*
- 19: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1998.DAT;*
- 20: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA1999.DAT;*
- 21: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2000.DAT;*
- 22: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2001.DAT;*
- 23: /SIDS1/gcdata/geneseq/geneseqp-emb1/AA2002.DAT;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	45	100.0	9	AAB37455	Human kininogen D3
2	45	100.0	10	AAY5405	Anti-angiogenic D3
3	45	100.0	16	AAY5409	Anti-angiogenic D3
4	45	100.0	16	AAY5410	Anti-angiogenic D3
5	45	100.0	32	AAY5408	Anti-angiogenic D3
6	45	100.0	117	AAR3350	Domaine 3, bradykinin
7	45	100.0	122	AAB3747	Human kininogen D3
8	45	100.0	123	AAY5426	Human high mol. wt.
9	45	100.0	248	ABG21102	Novel human diagno-
10	45	100.0	369	ABG21099	Novel human diagno-

PP	20-APR-2000: 2000W0-GB01571.
XX	PR 22-APR-1999; 99GB-009133.
XX	PA (BABR-) BABRAHAM INST.
XX	PA Human kininogen D3
XX	PI Anti-angiogenic D3
XX	XX Anti-angiogenic D3
XX	DR WPI: 2000-687316/67.
XX	PT Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of cystatin -
XX	PT Partial macaque platelet-a
PS Disclosure; Fig 4; 45pp; English.	PS

Human high molecular
Novel human diagno-
Human high molecular
Bradykinin analogo-
Human polypeptide
Human colon cancer
Novel human connec-
Lactococcus lactic
Staphylococcus hom-
Escherichia coli P
Bacillus sp. GUS P
Bacillus sp. GUS P
Bacillus sp. codon
Bacillus sp. GUS P
Staphylococcus bet-
Codon-optimised ST
Bacillus sp. GUS P
Human immune/haema
Arabidopsis thalia
Arabidopsis thalia
Drosophila melanog
Human secreted pro-
Human immune/haema
Human secreted pro-
Human mutant cysta-
Human mutant cysta-
Human protein which is s-
Human ORF-X protein
Human polypeptide
Novel human diagno-
Macaque Platelet-a
Macaque Platelet-a
Macaque partial pi-
Partial macaque pi-

ALIGNMENTS

RESULT 1
AAB37455 standard; peptide; 9 AA.
ID AAB7455 peptide fragment.
XX AC AAB37455;
XX DT 21-FEB-2001 (first entry)
XX DE Human kininogen D3 peptide fragment.
XX KW Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
XX OS Homo sapiens.
XX PN WO200064945-A1.
XX PD 02-NOV-2000.
XX XX

CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC the IC50 value for the present peptide was less than 0.8 uM for
 CC inhibition of fibroblast growth factor-induced HuVEC cell
 XX proliferation.

SQ Sequence 16 AA;

Query Match 100.0%; Score 45; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.099;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

Db 9 NNATFYFK 16

RESULT 5

ID AAY95408 standard; Peptide: 32 AA.

XX

AC AAY95410;

XX

DT 25-SEP-2000 (first entry)

XX

DE Anti-angiogenic D3 peptide.

XX

XX

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytosstatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

XX

OS Homo sapiens.

XX

PN WO200035407-A2.

XX

PF 02-DEC-1999; 99WO-US28465.

XX

PR 16-DEC-1998; 98US-0112427.

XX

WPI; 2000-442247/38.

XX

PA (UTEM) UNIV TEMPLE.

XX

PA (MCCR/) MCCRAE R K.

XX

PI McCrae RK;

XX

PT 22-JUN-2000.

XX

PT 02-DEC-1999; 99WO-US28465.

XX

PT 16-DEC-1998; 98US-0112427.

XX

PA (UTEM) UNIV TEMPLE.

XX

PA (MCCR/) MCCRAE R K.

XX

PI McCrae RK;

XX

WPI; 2000-442247/38.

XX

PS Claim 4; Page 26; 44pp; English.

XX

CC The present sequence is that of a D3 peptide derived from human

CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide

CC inhibits endothelial cell proliferation and thus possesses

CC anti-angiogenic activity. It is an example of D3 peptides of the

CC invention (see AAY95405-26) that are analogues of certain sites in

CC the HK domain 3, in this case amino acid residues Asn275-Lys282.

CC The peptides inhibit endothelial cell proliferation and may also

CC induce endothelial cell apoptosis. Compositions including the

CC peptides are used in claimed methods for inhibiting angiogenesis,

CC inhibiting endothelial cell proliferation, and inducing endothelial

CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders

CC characterized by undesired vascularization of the retina are treated.

CC the IC50 value for the present peptide was less than 0.8 uM for

CC inhibition of fibroblast growth factor-induced HuVEC cell

CC proliferation.

CC SQ Sequence 16 AA;

Query Match 100.0%; Score 45; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.099;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

Db 1 NNATFYFK 8

CC RESULT 4

ID AAY95410 standard; Peptide: 16 AA.

XX

AC AAY95410;

XX

DT 25-SEP-2000 (first entry)

XX

DE Anti-angiogenic D3 peptide.

XX

XX

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytosstatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

XX

OS Homo sapiens.

XX

PN WO200035407-A2.

XX

PD 22-JUN-2000.

XX

PF 02-DEC-1999; 99WO-US28465.

XX

PR 16-DEC-1998; 98US-0112427.

XX

WPI; 2000-442247/38.

XX

PA (UTEM) UNIV TEMPLE.

XX

PA (MCCR/) MCCRAE R K.

XX

PI McCrae RK;

XX

WPI; 2000-442247/38.

XX

PS Claim 4; Page 26; 44pp; English.

XX

CC The present sequence is that of a D3 peptide derived from human

CC high mol.wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide

CC inhibits endothelial cell proliferation and thus possesses

CC anti-angiogenic activity. It is an example of D3 peptides of the

CC invention (see AAY95405-26) that are analogues of certain sites in

CC the HK domain 3, in this case amino acid residues Asn275-Lys282.

CC The peptides inhibit endothelial cell apoptosis and may also

CC induce endothelial cell apoptosis. Compositions including the

CC peptides are used in claimed methods for inhibiting angiogenesis,

CC inhibiting endothelial cell proliferation, and inducing endothelial

CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders

CC characterized by undesired vascularization of the retina are treated.

CC the IC50 value for the present peptide was less than 0.8 uM for

CC inhibition of fibroblast growth factor-induced HuVEC cell

CC proliferation.

CC SQ Sequence 16 AA;

Query Match 100.0%; Score 45; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

||| | | | |

Db 13 NNATFYFK 20
RESULT 6
 AAR33350 ID AAR33350 standard; protein; 117 AA.
 XX AC AAR33350;
 XX DT 01-JUL-1993 (first entry)
 XX DE Domaine 3, bradykinin release activating peptide.
 XX KW Domain 3; human; kininogen; heavy chain; low molecular weight; plasma; trypsin; platelet; activation; granule contents; hemostasis; thrombin; tissue plasminogen activator; thrombosis; inflammatory response;
 XX KW Endothelial cell; von Willebrand factor;
 OS Homo sapiens.
 XX Key FH
 Peptide FT Location/Qualifiers
 FT /note= "Leader peptide"
 Protein FT 1..18
 FT /note= "Mature protein"
 XX PN WO9303748-A.
 PD 04-MAR-1993.
 XX PF 13-AUG-1992; 92WO-US06809.
 PR 13-AUG-1991; 91US-0744545.
 XX PA (UTEM) UNIV TEMPLE.
 XX PI Jiang Y, Schmaier AB;
 XX WPI; 1993-093714/11.
 XX PT Use of trypsin-cleavage fragment of human kininogen - for increasing vascular bradykinin release, for lowering blood pressure and treating hypertension
 XX PS Disclosure: Fig 1; 46pp; English.
 XX SQ Sequence 117 AA;
 CC The sequence given represents domain 3, amino acids 246-362, of the human kininogen heavy chain. Domain 3 was isolated from low molecular weight kininogen, derived from human plasma, by cleavage with trypsin. Domain 3 peptide inhibits platelet activation causing a marked decrease in the platelets ability to aggregate and secrete their granule contents. The granule contents comprise proteins which participate in hemostasis, thrombosis and the inflammatory response. Domain 3 also inhibits endothelial cell activation shown by a decrease in secretion of endothelial cell contents such as tissue plasminogen activator and von Willebrand factor. Domain 3 functions to inhibit cell activation by blocking thrombin binding to its target cells, the peptide is a selective inhibitor of thrombin-induced platelet activation.
 XX SQ Sequence 117 AA;
 Query Match 1 NNATFYFK 8
 Best Local Similarity 100.0%; Score 45; DB 14; Length 117;
 Matches 8; Conservative 0; Mismatches 0; Gaps 0;
 XX AC AAY95426;
 XX DT 25-SEP-2000 (first entry)
 XX DE Human high mol.wt. kininogen domain 3.
 XX KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 XX KW rheumatoid arthritis; cyostatic; antilarritic; antirheumatic; therapy; human; D3 peptide.
 OS Homo sapiens.
 XX PN WO200035407-A2.
 XX PD 22-JUN-2000.
 XX PR 02-DEC-1999; 99WO-US28465.

Db 13 NNATFYFK 20
RESULT 7
 AAB37447

XX PR 16-DEC-1998; 98US-0112427.
 XX PA (UNIV) UNIV TEMPLE.
 PA (MCCR/) MCCRAE R K.
 XX PI McCrae RK;
 XX WPI; 2000-442247/38.
 XX Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3 analog -
 DR Disclosure; Page 4; 44pp; English.
 XX The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention relates to isolated polynucleotide sequences (see AAY95405-24) that are analogues of certain sites in the HK domain 3, specifically Asn275-Lys382, Cys246-Cys249, Lys331-Tyr338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer, rheumatoïd arthritis, and ocular disorders characterized by undesired vascularization of the retina are treated.
 XX Sequence 123 AA;
 SQ Query Match 100.0%; Score 45; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNATFYFK 8
 Db 41 NNATFYFK 4.8
 XX RESULT 9
 AC ABG21102 standard; Protein: 248 AA.
 XX DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #21093.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic; KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PR 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS85239.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 XX PS Claim 20; SEQ ID No 51461; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published.pct_sequences.
 SQ Sequence 248 AA;
 Query Match 100.0%; Score 45; DB 22; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNATFYFK 8
 Db 90 NNATFYFK 97
 XX RESULT 10
 AC ABG21099
 XX ID ABG21099 standard; Protein: 369 AA.
 AC ABG21099;
 XX DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #21090.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic; KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PR 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX DR WPI; 2001-639362/73.
 DR N-PSDB; AAS85239.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PT	Novel human kininogen D5 domain polypeptides useful for treating									
XX	conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign hyperplasia									
XX	Disclosure; Page 13; 84pp; English.									
PS	The invention relates to isolated polynucleotide (I) and									
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,									
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome									
CC	and gene mapping, and in recombinant production of (III). The									
CC	polynucleotides are also used in diagnostics as expressed sequence tags									
CC	for identifying expressed genes. (I) is useful in gene therapy techniques									
CC	to restore normal activity of (II) or to treat disease states involving									
CC	(III) is useful for generating antibodies against it, detecting or									
CC	quantitating a polypeptide in tissue, as molecular weight markers and as									
CC	a food supplement. (II) and its binding partners are useful in medical									
CC	imaging of sites expressing (III). (I) and (II) are useful for treating									
CC	disorders involving aberrant protein expression or biological activity.									
CC	the polypeptide and polynucleotide sequences have applications in									
CC	diagnostics, forensics, gene mapping, identification of mutations									
CC	responsible for genetic disorders or other traits to assess biodiversity									
CC	and to produce other types of data and products dependent on DNA and									
CC	amino acid sequences. ABG0010-ABG3077 represent novel human									
CC	diagnostic amino acid sequences of the invention.									
CC	Note: The sequence data for this patent did not appear in the printed									
CC	specification, but was obtained in electronic format directly from WIPO									
CC	at ftp.wipo.int/pub/published_pct_sequences .									
Sequence	369 AA;									
Query	1 NNATPFYK 8	Score	100.0%	DB	22;	Length	369;			
Matches	Best Local Similarity	100.0%	Pred. No.	2.5;						
Db	333 NNATPFYK 340	Mismatches	0;	Indels	0;	Gaps	0;			
RESULT 11		Query	1 NNATPFYK 8	Match	1	Score	45;	DB	23;	Length
ABR7B/07	ID	ABR7B/07	standard	Local	100.0%	Pred. No.	4.3;	26;		
XX	XX	XX	Protein	Matches	8;	Conservative	0;	Mismatches	0;	Gaps
Qy	1 NNATPFYK 8	Sequence	626 AA;	Indels	0;	Gaps	0;			
Db	333 NNATPFYK 340	SQ								
RESULT 12		Query	1 NNATPFYK 8	Match	1	Score	45;	DB	23;	Length
ABG21101	ID	ABG21101	standard	Local	100.0%	Pred. No.	4.3;	26;		
XX	XX	XX	Protein	Matches	8;	Conservative	0;	Mismatches	0;	Gaps
AC	AC	AC	Sequence	626 AA;	Indels	0;	Gaps	0;		
ABG21101;		Db	275 NNATPFYK 282							
RESULT 13		Query	1 NNATPFYK 8	Match	1	Score	45;	DB	23;	Length
DT	DT	DT	Protein	Local	100.0%	Pred. No.	4.3;	26;		
DB	DB	DB	Sequence	626 AA;	Indels	0;	Gaps	0;		
Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human
kininogen	kininogen	kininogen	kininogen	kininogen	kininogen	kininogen	kininogen	kininogen	kininogen	kininogen
high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight	high molecular weight
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
D5 receptor;	angiogenesis;	endothelial cell;	cystostatic;	antitumour;						
antiatherosclerotic;	vasoconstrictor;	vulnerability;	transquiliser;	thrombolytic;						
vascular;	vasoconstrictor;	transquiliser;	thrombolytic;	antiarteritic;						
gynaecological;	gynaecological;	gynaecological;	gynaecological;	antiarteritic;						
antiangiogenic;	antiangiogenic;	antiangiogenic;	antiangiogenic;	apoptosis;						
XX	XX	XX	XX	XX	XX	XX	XX	XX	XX	XX
Homo sapiens.	OS	Location/Qualifiers								
Key	Domain	348 .. 508	/label=	D5_domain						
XX	XX	XX								
WO200314369-A2.										
XX	XX	XX								
PD	PD	PD	21-FEB-2002.							
XX	XX	XX	24-JUL-2001;	2001WO-US23185.						
PF	PF	PF	24-JUL-2000;	2000US-220194P.						
XX	XX	XX	(ATT-E)	ATTENION LLC.						
PA	PA	PA	Mazar AP,	Juarez JC;						
XX	XX	XX	WPI:	2002-393611/42.						
DR	DR	DR	N-PSDB;	AAS8288.						
XX	XX	XX	WPI:	2001-639162/73.						

PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsive for genetic disorders or other traits and to assess biodiversity -	XX	FT	/label= D5_domain
PT	Claim 20; SEQ ID No 51460; 103pp; English.	XX	PN	WO200214369-A2.
PS	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome, and gene mapping, and in recombinant production of (III). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.	XX	XX	21-FEB-2002.
CC	Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .	XX	XX	PD 24-JUL-2001; 2001WO-US23185.
CC	Sequence 644 AA;	XX	XX	PR 24-JUL-2000; 2000US-220194P.
CC	Query Match Score 45; DB 22; Length 644; Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;	XX	XX	PA (ATE-) ATTENON LLC.
CC	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	Mazar AP, Juarez JC; WPI; 2002-395611/42.
CC	QY 1 NNATFYFK 8	XX	XX	Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign hyperplasia
CC	Db 293 NNATFYFK 300	XX	XX	DR Disclosure; FIG 1B-E; 84pp; English.
CC	RESULT 13	XX	XX	PS The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kininogen, or biologically active peptide fragment, homologue or functional derivative, and which: (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required for maintenance of EC viability. (I) has cytostatic, antitumour, antiatherosclerotic, vasotropic, pulmonary, tranquilliser, thrombolytic, ophthalmological, gynaecological, antidiabetic, antiarthritic, antiangiogenic, antiapoptotic and endocrine activities.
CC	ABB78710 standard; Protein: 644 AA.	XX	XX	CC An antibody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide (II) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X) comprising (I), (II), or (III), can be used for treating a subject having a disease or condition associated with undesired EC migration, proliferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the human high molecular weight kininogen (HK) protein, which is given in the exemplification of the present invention.
CC	ABB78710; AC ABB78710; DT 18-JUL-2002 (first entry)	XX	XX	CC Sequence 644 AA;
DE	Human high molecular weight kininogen (HK) protein.	XX	XX	CC Query Match Score 45; DB 23; Length 644; Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Indels 0; Gaps 0;
KW	Human; kininogen; high molecular weight kininogen; HK; D5 domain; DS Receptor; angiogenesis; endothelial cell; cytosolic; antitumour; antiatherosclerotic; vasotropic; pulmonary; tranquilliser; thrombolytic; ophthalmological; gynaecological; antidiabetic; antiarthritic; antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.	XX	QY 1 NNATFYFK 8	AC AAN54336;
XX	Homo sapiens.	XX	Db 293 NNATFYFK 300	XX 30-JUL-1998 (first entry)
XX	Key Location/Qualifiers	XX	XX	Bradykinin analogous peptide 19.
FH	Peptide 1..18	XX	XX	Inhibition; thrombin-induced platelet; prevention; platelet aggregation;
FT	FT /label= signal	XX	XX	KW ADP-induced activation.
FT	Protein 19..644	XX	XX	OS Synthetic.
FT	FT /label= mature_human_high_molecular_weight_kininogen	XX	XX	FT
FT	Disulfide-bond 28..614	XX	XX	FT
FT	Disulfide-bond 83..94	XX	XX	FT
FT	Disulfide-bond 107..126	XX	XX	FT
FT	Disulfide-bond 142..145	XX	XX	FT
FT	Disulfide-bond 206..218	XX	XX	FT
FT	Disulfide-bond 229..248	XX	XX	FT
FT	Disulfide-bond 264..267	XX	XX	FT
FT	Disulfide-bond 328..340	XX	XX	FT
FT	Disulfide-bond 351..370	XX	XX	FT
FT	Domain 402..526	XX	XX	FT

PN WO9641640-A1.
 XX
 PD 27-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US09940.
 XX PR 09-JUN-1995; 95US-0000096.
 XX PA (UNMI) UNIV MICHIGAN.
 XX PI Hasan AAK, Schmaier AH;
 XX DR; 1997-06530/06.
 XX PR Inhibition of platelet activation and aggregation - by admin. of new or known bradykinin analogues
 XX Disclosure: Page 44; 73pp; English.
 PS Sequence: 26 AA;
 CC Administration of a peptide or multimer related to bradykinin or other disclosed peptides and multimers can be used for the inhibition of thrombin-induced platelets or other cells. They can also be used for preventing platelet aggregation, or inhibiting ADP-induced activation. This is useful to prevent arterial occlusions arising from coronary thrombosis and stroke.
 XX Sequence 26 AA;
 CC
 CC

Query Match 86.7%; Score 39; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
 Db 1 NATFYFK 7

RESULT 15
 AAO05080
 ID AAO05080 standard; Protein: 78 AA.
 XX AC AAO05080;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 18972.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide; stem cell growth factor; haematoopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PP 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-0515126.
 PR 18-MAY-2000; 2000US-0577409.
 XX PA (HYSE) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-514838/56.
 DR N-PSDB; AAI85011.
 XX PR Isolated nucleic acids and polypeptides, useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders.

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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:57 ; Search time 7.66667 Seconds
(without alignments)
30.702 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45

Sequence: 1 NNATEYFK 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942922 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
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3: /cgn2_6/ptodata/2/iaa/6A_COMBO.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	45	100.0	117	1	US-08-193-114B-1	Sequence 1, Appli
2	45	100.0	117	5	PCT-US92-06809-1	Sequence 1, Appli
3	39	86.7	26	4	US-08-676-242-15	Sequence 2, Appli
4	34	75.6	602	4	US-09-149-727-2	Sequence 8, Appli
5	34	75.6	607	4	US-09-149-727-8	Sequence 4, Appli
6	34	75.6	618	4	US-09-149-727-4	Sequence 30, Appli
7	31	68.9	193	2	US-08-485-938A-36	Sequence 36, Appli
8	31	68.9	441	1	US-08-318-905-8	Sequence 8, Appli
9	31	68.9	441	1	US-08-328-474-8	Sequence 8, Appli
10	31	68.9	441	1	US-09-100-546-8	Sequence 8, Appli
11	31	68.9	441	1	US-08-483-232-8	Sequence 8, Appli
12	31	68.9	441	1	US-08-140-140-8	Sequence 8, Appli
13	31	68.9	441	2	US-08-485-938A-8	Sequence 8, Appli
14	31	68.9	441	2	US-08-910-041-8	Sequence 8, Appli
15	31	68.9	441	3	US-09-328-474-8	Sequence 8, Appli
16	31	68.9	441	3	US-08-100-546-8	Sequence 8, Appli
17	31	68.9	441	4	US-09-010-715-8	Sequence 8, Appli
18	31	68.9	441	4	US-09-577-758-4	Sequence 8, Appli
19	31	68.9	444	1	US-08-483-140-28	Sequence 28, Appli
20	31	68.9	444	2	US-08-485-938A-32	Sequence 32, Appli
21	31	68.9	902	1	US-08-701-846-2	Sequence 6, Appli
22	31	68.9	2710	2	US-08-480-604A-6	Sequence 6, Appli
23	31	68.9	2710	2	US-08-405-496A-6	Sequence 6, Appli
24	31	68.9	2710	4	US-08-915-136-6	Sequence 6, Appli
25	31	68.9	2710	4	US-08-957-310-6	Sequence 6, Appli
26	30	66.7	84	4	US-09-227-357-597	Sequence 597, App
27	30	66.7	572	6	5200183-5	Patent No. 5200183

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29	30	66.7	602	3	US-08-446-100-2	Sequence 2, Appli
30	30	66.7	602	3	US-08-446-100-3	Sequence 3, Appli
31	30	66.7	602	3	US-08-446-100-4	Sequence 4, Appli
32	30	66.7	602	3	US-08-446-100-5	Sequence 5, Appli
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36	30	66.7	602	3	US-08-446-100-9	Sequence 9, Appli
37	30	66.7	602	3	US-08-446-100-10	Sequence 10, Appli
38	30	66.7	602	3	US-08-446-100-11	Sequence 11, Appli
39	30	66.7	602	3	US-08-446-100-12	Sequence 12, Appli
40	30	66.7	602	3	US-08-446-100-13	Sequence 13, Appli
41	30	66.7	602	3	US-08-446-100-14	Sequence 14, Appli
42	30	66.7	602	3	US-08-446-100-15	Sequence 15, Appli
43	30	66.7	602	3	US-08-446-100-16	Sequence 16, Appli
44	30	66.7	602	3	US-08-446-100-17	Sequence 17, Appli
45	30	66.7	602	3	US-08-446-100-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1	US-08-193-114B-1	US/08193114B	Application US/08193114B
		; Patent No. 5472445	
		; GENERAL INFORMATION:	
		; APPLICANT: Schmalier, Alvin H.	
		; ATTORNEY: Jiang, Yongping	
		; TITLE OF INVENTION: Modulation of Blood Pressure and Inhibition of Platelet Activation	
		; TITLE OF INVENTION: with Kininogen Fragment	
		; NUMBER OF SEQUENCES: 2	
		; CORRESPONDENCE ADDRESS:	
		; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.	
		; STREET: 1800 Two Penn Center Plaza	
		; CITY: Philadelphia	
		; STATE: Pennsylvania	
		; ZIP: 19102	
		; COMPUTER READABLE FORM:	
		; COMPUTER: IBM PS/2	
		; OPERATING SYSTEM: MS-DOS	
		; SOFTWARE: Wordperfect 5.1	
		; CURRENT APPLICATION DATA:	
		; APPLICATION NUMBER: US08193114B	
		; FILING DATE: 9 February 1994	
		; CLASSIFICATION: 514	
		; PRIOR APPLICATION DATA:	
		; APPLICATION NUMBER: U.S. Application	
		; APPLICATION NUMBER: Serial No. 5472945 07/744,545	
		; FILING DATE: 13 August 1991	
		; ATTORNEY/AGENT INFORMATION:	
		; NAME: Monaco, Daniel A.	
		; REGISTRATION NUMBER: 30,480	
		; REFERENCE/DOCKET NUMBER: 6056-137 C11	
		; TELECOMMUNICATION INFORMATION:	
		; TELEPHONE: (215) 568-8383	
		; TELEFAX: (215) 568-5549	
		; TELEX: No. 5472945e	
		; INFORMATION FOR SEQ ID NO: 1:	
		; SEQUENCE CHARACTERISTICS:	
		; LENGTH: 117 amino acids	
		; TYPE: peptide	
		; TOPOLOGY: linear	
		; US-08-193-114B-1	
		Query Match 8 Score 45; DB 1; Length 117;	
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; Sequence 1, Application PC/TUUS9206809
; GENERAL INFORMATION:
;   APPLICANT: Schmaier, Alvin H.
;   APPLICANT: Jiang, Yongping
;   TITLE OF INVENTION: Modulation of Blood
;   TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
;   NUMBER OF SEQUENCES: 2
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WordPerfect 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/TUUS92/06809
;     FILING DATE: 19910813
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: U.S. Application
;     APPLICATION NUMBER: Serial No. 744,545
;     FILING DATE: 13 August 1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Moroco, Daniel A.
;     REGISTRATION NUMBER: 30,480
;     REFERENCE/DOCKET NUMBER: 6056-137
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (215) 568-8883
;     TELEFAX: (215) 568-5549
;     TELEX:
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 117 amino acids
;     TYPE: AMINO ACID
;     TOPOLOGY: linear
; PCT-US92-06809-1

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Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   30 NNATFYFK 37

RESULT 3
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; Sequence 15, Application US/08676242C
; GENERAL INFORMATION:
;   APPLICANT: The Regents of the University of Michigan
;   APPLICANT: Schmaier, Alvin H.
;   APPLICANT: Hasan, Ahmed A.K.
;   TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
;   FILE REFERENCE: 8820-2 US
;   CURRENT APPLICATION NUMBER: US/08/676,242C
;   CURRENT FILING DATE: 2000-07-16

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Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-149-727-2
; Sequence 2, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
;   APPLICANT: Jefferson, Richard A.
;   APPLICANT: Kilian, Andrzej
;   APPLICANT: Keese, Paul Konrad
;   TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 190106 405
;   CURRENT APPLICATION NUMBER: US/09/149,727
;   CURRENT FILING DATE: 1998-09-08
;   EARLIER APPLICATION NUMBER: US 60/058,263
;   EARLIER FILING DATE: 1997-09-09
;   NUMBER OF SEQ ID NOS: 71
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Bacillus sp.
;   US-09-149-727-2

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Best Local Similarity 100.0%; Pred. No. 0.5; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-149-727-8
; Sequence 8, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
;   APPLICANT: Jefferson, Richard A.
;   APPLICANT: Kilian, Andrzej
;   TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 190106 405
;   CURRENT APPLICATION NUMBER: US/09/149,727
;   CURRENT FILING DATE: 1998-09-08
;   EARLIER APPLICATION NUMBER: US 60/058,263
;   EARLIER FILING DATE: 1997-09-09
;   NUMBER OF SEQ ID NOS: 71
;   SOFTWARE: PatentIn Ver. 2.0
;   SEQ ID NO 2
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Bacillus sp.
;   US-09-149-727-8

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Best Local Similarity 75.0%; Pred. No. 90; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-149-727-9
; Sequence 9, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
;   APPLICANT: Keese, Paul Konrad
;   TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: 190106 405
;   CURRENT APPLICATION NUMBER: US/09/149,727
;   CURRENT FILING DATE: 1998-09-08
;   EARLIER APPLICATION NUMBER: US 60/058,263
;   EARLIER FILING DATE: 1997-09-09
;   NUMBER OF SEQ ID NOS: 71
;   SOFTWARE: PatentIn Ver. 2.0
;   US-09-149-727-9
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SEQ ID NO 8
 LENGTH: 607
 TYPE: PRT
 ORGANISM: *Bacillus* sp.
 US-09-149-727-8

Query Match Score 34; DB 4; Length 607;
 Best Local Similarity 75.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
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RESULT 6
 US-09-149-727-4
 ; Sequence 4, Application US/09149727
 ; GENERAL INFORMATION:
 ; APPLICANT: Killian, Andrae J.
 ; APPLICANT: Jefferson, Richard A.
 ; APPLICANT: Keese, Paul Konrad
 ; TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND FILE REFERENCE: 190106 405
 ; CURRENT APPLICATION NUMBER: US/09/149,727
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: US 60/058,263
 ; EARLIER FILING DATE: 1997-09-09
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 618
 ; TYPE: PRT
 ; ORGANISM: *Bacillus* sp.
 US-09-149-727-4

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 Best Local Similarity 75.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
 Db 304 NNKPFYFK 311

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 ; Sequence 30, Application US/08483140
 ; Patent No. 5698403
 ; GENERAL INFORMATION:
 ; APPLICANT: ICOS Corporation
 ; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
 ; TITLE OF INVENTION: Hydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,140
 ; FILING DATE: 08-09-1998
 ; CLASSIFICATION: 435
 ; PRIORITY DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5847088and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 32781
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 193 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 US-08-483-140-30

Query Match Score 31; DB 1; Length 193;
 Best Local Similarity 71.4%; Pred. No. 1e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYFK 8
 Db 143 SATYFYK 149

RESULT 8
 US-08-485-938A-36
 ; Sequence 36, Application US/08485938A
 ; Patent No. 5847088
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousins, Lawrence S.
 ; Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Ha I.
 ; APPLICANT: Thielker, Larry W.
 ; APPLICANT: Wilder, Cheyrel L.
 ; TITLE OF INVENTION: Platelet Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
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 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
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 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIORITY DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5847088and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/32792
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEX: (312) 474-0448

TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-36

RESULT 10
US-08-318-905-B
; Sequence 8, Application US/08318905
; Patent No. 5611669
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5611669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-905-B

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

RESULT 11
US-08-483-232-B
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 26

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 NATFYFK 8
Db 185 SATYFK 191

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 2 NATFYFK 8
Db 185 SATYFK 191

NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483-232
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INVENTORY FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-232-8

Query Match 68.9%; Score 31; DB 1; Length 441;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATYYFK 8
Db 185 SATYYFK 191

RESULT 12
US-08-483-140-8
; Sequence 8, Application US/08483140
; GENERAL INFORMATION:
; APPLICANT: ICGS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483-140
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300

Fri Mar 14 09:20:26 2003

us-09-461-061a-1.rai

Page 7

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Title: US-09-461-061a-1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	8
1	34	75.6	61	10	US-09-764-847-566	Sequence 566, App	
2	32	71.1	1659	10	US-09-801-368-118	Sequence 118, App	
3	31	68.9	178	9	US-09-768-235B-6	Sequence 6, Appli	
4	31	68.9	224	10	US-09-815-242-13997	Sequence 8, Appli	
5	31	68.9	441	10	US-09-729-402-8	Sequence 10, Appli	
6	31	68.9	1114	10	US-09-740-046-10	Sequence 158, App	
7	30	66.7	84	9	US-09-983-802-597	Sequence 597, App	
8	30	66.7	82	9	US-09-510-332-99	Sequence 332, App	
9	30	66.7	84	9	US-09-510-33-155	Sequence 155, App	
10	30	66.7	127	10	US-09-780-053-5	Sequence 5, Appli	
11	30	66.7	183	10	US-09-801-368-336	Sequence 336, App	
12	30	66.7	307	10	US-09-825-882-18	Sequence 518, App	
13	30	66.7	308	9	US-09-510-332-99	Sequence 99, App	
14	30	66.7	308	9	US-09-510-33-155	Sequence 155, App	
15	30	66.7	351	10	US-09-780-053-5	Sequence 5, Appli	
16	30	66.7	452	10	US-09-801-368-336	Sequence 336, App	
17	30	66.7	545	9	US-09-826-5134	Sequence 5134, App	
18	30	66.7	574	10	US-09-748-739A-4	Sequence 4, Appli	
19	30	66.7	574	10	US-09-748-739A-5	Sequence 6, Appli	
					US-09-748-739A-8	Sequence 8, Appli	

ALIGNMENTS

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RESULT 1
US-09-764-847-566
; Sequence 566, Application US/09764847
; Patent No. US200213276A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 566
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-847-566
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Query Match 75.6%; Score 34; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-801-368-118
; Sequence 118, Application US/09801368
; Patent No. US200212855A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: Thea
```

Query Match 1 NNAATFVFK 8
 Best Local Similarity 71.1%; Pred. No. 3.9e+02; Length 1659;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
 US-09-768-235B-6
 Sequence 6, Application US/09768235B
 Publication No. US2003002400A1
 GENERAL INFORMATION:
 ; APPLICANT: Frank, Marcus
 ; APPLICANT: Reindl, Andreas
 ; APPLICANT: Schmidt, Ralf-Michael
 ; APPLICANT: Freund, Annette
 ; APPLICANT: Ehrhardt, Thomas
 ; APPLICANT: Bischoff, Friedrich
 ; APPLICANT: Renz, Andreas
 ; APPLICANT: Duweling, Elke
 ; APPLICANT: Cirpus, Petra
 ; APPLICANT: Lerchel, Jens
 ; APPLICANT: Reski, Ralf
 ; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved in the regulation of cell division, growth and biomass formation in plants
 ; FILE REFERENCE: 0093/00009
 ; CURRENT APPLICATION NUMBER: US/09768-235B
 ; CURRENT FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: PCT/EP00/00675
 ; PRIOR FILING DATE: 2000-01-28
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 2.1/WordPerfect version 6.1
 ; SEQ ID NO: 6
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: *Physcomitrella patens*
 ; US-09-801-368-118

Query Match 1 NNAATFVFK 342
 Best Local Similarity 75.0%; Pred. No. 3.9e+02; Length 1659;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 3
 US-09-768-235B-6
 Sequence 6, Application US/09768235B
 Publication No. US2003002400A1
 GENERAL INFORMATION:
 ; APPLICANT: Frank, Marcus
 ; APPLICANT: Reindl, Andreas
 ; APPLICANT: Schmidt, Ralf-Michael
 ; APPLICANT: Freund, Annette
 ; APPLICANT: Ehrhardt, Thomas
 ; APPLICANT: Bischoff, Friedrich
 ; APPLICANT: Renz, Andreas
 ; APPLICANT: Duweling, Elke
 ; APPLICANT: Cirpus, Petra
 ; APPLICANT: Lerchel, Jens
 ; APPLICANT: Reski, Ralf
 ; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involved in the regulation of cell division, growth and biomass formation in plants
 ; FILE REFERENCE: 0093/00009
 ; CURRENT APPLICATION NUMBER: US/09768-235B
 ; CURRENT FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: PCT/EP00/00675
 ; PRIOR FILING DATE: 2000-01-28
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 2.1/WordPerfect version 6.1
 ; SEQ ID NO: 6
 ; LENGTH: 178
 ; TYPE: PRT
 ; ORGANISM: *Physcomitrella patens*
 ; US-09-768-235B-6

Query Match 1 NNAATFVFK 79
 Best Local Similarity 68.9%; Pred. No. 70; Length 178;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 4
 US-09-815-242-13997
 Sequence 4, Application US/09815242
 ; Sequence 4, Application US/09815242

; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 ; FILE REFERENCE: ELITRA_011A
 ; CURRENT APPLICATION NUMBER: US/09815, 242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIORITY NUMBER: 60/191,078
 ; PRIORITY FILING DATE: 2000-03-21
 ; PRIORITY APPLICATION NUMBER: 60/206,848
 ; PRIORITY FILING DATE: 2000-05-23
 ; PRIORITY APPLICATION NUMBER: 60/207,727
 ; PRIORITY FILING DATE: 2000-05-26
 ; PRIORITY APPLICATION NUMBER: 60/242,578
 ; PRIORITY FILING DATE: 2000-10-23
 ; PRIORITY APPLICATION NUMBER: 60/253,625
 ; PRIORITY FILING DATE: 2000-11-27
 ; PRIORITY APPLICATION NUMBER: 60/257,931
 ; PRIORITY FILING DATE: 2000-12-22
 ; PRIORITY APPLICATION NUMBER: 60/259,308
 ; PRIORITY FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 13997
 ; LENGTH: 224
 ; TYPE: PRT
 ; ORGANISM: *Salmonella typhi*
 ; US-09-815-242-13997
 ; Query Match 1 NNAATFVFK 7
 ; Best Local Similarity 68.9%;
 ; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 ; Qy 1 NNAATFVFK 7
 ; Db 1: 1: 1
 ; Db 28 NNSLFYF 34
 ; RESULT 5
 ; US-09-729-402-8
 ; Sequence 8, Application US/09729402
 ; Patent No. US20010021379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousins, Lawrence S.
 ; Eberhardt, Christine D.
 ; Gray, Patrick W.
 ; Le Trong, Hai
 ; Tjoelker, Larry W.
 ; Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; ACetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:


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; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,.949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,.947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,.684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,.661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 597
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-597

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Query Match 66.7%; Score 30; DB 9; Length 84;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Oy 2 NATFYF 7
Db 60 NATFFF 65

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RESULT 9
US-09-764-853-756
; Sequence 756, Application US/09764853
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764, 853
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 756
; LENGTH: 127
; TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011307.1
; SEQ ID NO: 35808
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6

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; ; ORGANISM: Homo sapiens
; ; US-09-764-853-756
; ; Query Match 66.7%; Score 30; DB 10; Length 127;
; ; Best Local Similarity 71.4%; Pred. No. 77;
; ; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; ; Qy 1 NNATFYF 7
; ; Db 66 NNNTLYF 72
; ; RESULT 10
; ; US-09-864-761-35808
; ; Sequence 35808, Application US/09864761
; ; Patent No. US2002004873A1
; ; GENERAL INFORMATION:
; ; APPLICANT: Penn, Sharron G.
; ; APPLICANT: Rank, David R.
; ; APPLICANT: Hanzel, David K.
; ; APPLICANT: Chen, Wenshenq
; ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; ; FILE REFERENCE: Aeomica-X-1
; ; CURRENT APPLICATION NUMBER: US/09/864,761
; ; CURRENT FILING DATE: 2001-05-23
; ; PRIOR APPLICATION NUMBER: US 60/180,312
; ; PRIOR FILING DATE: 2000-02-04
; ; PRIOR APPLICATION NUMBER: US 60/207,456
; ; PRIOR FILING DATE: 2000-05-26
; ; PRIOR APPLICATION NUMBER: US 09/632,366
; ; PRIOR FILING DATE: 2000-08-03
; ; PRIOR APPLICATION NUMBER: GB 24263 .6
; ; PRIOR FILING DATE: 2000-10-04
; ; PRIOR APPLICATION NUMBER: US 60/236,359
; ; PRIOR FILING DATE: 2000-09-27
; ; PRIOR APPLICATION NUMBER: PCT/US01/00666
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00667
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00664
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00669
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00665
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00668
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00663
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00662
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00661
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00670
; ; PRIOR FILING DATE: 2001-01-30
; ; PRIOR APPLICATION NUMBER: PCT/US01/00667
; ; PRIOR FILING DATE: 2000-09-21
; ; PRIOR APPLICATION NUMBER: US 09/608,408
; ; PRIOR FILING DATE: 2000-06-30
; ; PRIOR APPLICATION NUMBER: US 09/774,203
; ; PRIOR FILING DATE: 2001-01-29
; ; NUMBER OF SEQ ID NOS: 49117
; ; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; ; SEQ ID NO: 35808
; ; LENGTH: 183
; ; TYPE: PRT
; ; ORGANISM: Homo sapiens
; ; FEATURE:
; ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.3
; ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.3
; ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6

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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.6
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.6
 OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 7.9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.4
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.4
 OTHER INFORMATION: EXPRESSED IN BPA74, SIGNAL = 4.8
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.6
 OTHER INFORMATION: EST HUMAN HIT: AW937782-1, EVALUATE 7.00e-79
 OTHER INFORMATION: SWISSPROT HIT: Q35136, EVALUATE 8.00e-12
 US-09-864-761-35808

Query Match Score 30; DB 10; Length 181;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFFYF 7
 Db 112 NNATFFYF 118

RESULT 11
 US-09-825-882-18
 Sequence 18, Application US/098258882
 Patent No. US2003009451A1
 GENERAL INFORMATION:
 APPLICANT: ADLER, JON ELLIOT
 TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
 FILE REFERENCE: 078003/02/19152/RXT
 CURRENT APPLICATION NUMBER: US/09/825,882
 CURRENT FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/195,532
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: 60/247,014
 PRIOR FILING DATE: 2000-11-13
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 18
 LENGTH: 307
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-825-882-18

Query Match Score 30; DB 10; Length 307;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NNATFFYF 7
 Db 93 NSATFWF 99

RESULT 12
 US-09-510-332-99
 Sequence 99, Application US/09510332
 Publication No. US2003002278A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Adler, Jon Elliot
 APPLICANT: Ryba, Nick
 APPLICANT: Mueller, Ken
 APPLICANT: Hoon, Mark
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: T2R, a No. US2003002278A1 Family of Taste Receptors
 CURRENT APPLICATION NUMBER: US/09/510,332
 CURRENT FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 09/393,634
 PRIOR FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 172
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 155
 LENGTH: 308
 TYPE: PRT
 ORGANISM: Mus sp.
 FEATURE:
 OTHER INFORMATION: mouse T2R26 (mGR26)

Query Match Score 30; DB 9; Length 308;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFFYF 7
 Db 93 NSATFWF 99

RESULT 13
 US-09-510-332-155
 Sequence 155, Application US/09510332
 Publication No. US2003002278A1
 GENERAL INFORMATION:
 APPLICANT: Zuker, Charles S.
 APPLICANT: Adler, Jon Elliot
 APPLICANT: Ryba, Nick
 APPLICANT: Mueller, Ken
 APPLICANT: Hoon, Mark
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: T2R, a No. US2003002278A1 Family of Taste Receptors
 CURRENT APPLICATION NUMBER: US/09/510,332
 CURRENT FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: US 09/393,634
 PRIOR FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 172
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 155
 LENGTH: 308
 TYPE: PRT
 ORGANISM: Mus sp.
 FEATURE:
 OTHER INFORMATION: mouse T2R26 (mGR26)

Query Match Score 30; DB 9; Length 308;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFFYF 7
 Db 93 NSATFWF 99

RESULT 14
 US-09-780-053-5
 Sequence 5, Application US/09780053
 Publication No. US2003010264A1
 GENERAL INFORMATION:
 APPLICANT: Rene S. Hubert
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Pia M. Challita-Eld
 APPLICANT: Mary Faris
 APPLICANT: Elana Levin
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Aya Jakobovits
 APPLICANT: Ayala Jakobovits
 TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
 CURRENT APPLICATION NUMBER: US/09/780,053
 CURRENT FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/181,261
 PRIOR FILING DATE: 2001-02-09
 NUMBER OF SEQ ID NOS: 716
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 308

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; TYPE: PRT
; ORGANISM: Drosophila Melanogaster
US-09-780-033-5

Query Match      66.7%; Score 30; DB 10; Length 351;
Best Local Similarity    71.4%; Pred. No. 2.1e+02;
Matches      5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy          2 NATFYFK 8
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Db          272 NSTFYIK 278
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RESULT 15
US-09-801-368-336
; Sequence 336, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Calli, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sozie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 336
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-336
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Query Match      66.7%; Score 30; DB 10; Length 452;
Best Local Similarity    62.3%; Pred. No. 2.6e+02;
Matches      5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy          1 NNATFYFK 8
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Db          406 NNKTFPLK 413
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Search completed: March 13, 2003, 19:15:00
Job time: 8 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	427	1 KGHNLL	kininogen, LMW precursor [validated] - human
2	45	100.0	644	1 KGHNLL	N; Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen
3	39	86.7	433	2 A2B055	N; Contains: bradykinin (kallidin); kininogen I; prokininogen
4	39	86.7	639	2 A25486	C; Species: Homo sapiens (man)
5	36	80.0	858	2 T24062	C; Date: 06-Jul-1982 #sequence revision 27-Nov-1985 #text_change 08-Dec-2000
6	36	80.0	1132	2 T31107	C; Accession: A01280; A27900
7	35	77.8	182	2 T24206	A; Reference number: A90490; MUID:85122621; PMID:6441591
8	34	75.6	71	2 BB3803	A; Accession: A01280
9	34	75.6	182	2 T06978	A; Residues: 1-427 <OKH>
10	34	75.6	273	2 F86924	A; Cross-references: GB:K02566; NID:9177889; PIDN:AAA35497-1; PID:g177890
11	34	75.6	319	2 A6650	R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
12	34	75.6	440	2 T11319	R; Takagaki, Y.; Kitamura, N.; Nakaniishi, S.
13	34	75.6	497	2 G96611	Biochemistry 23, 5691-5697, 1984
14	34	75.6	630	2 T25830	A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
15	34	75.6	758	2 T31994	A; Reference number: A90490; MUID:85122621; PMID:6441591
16	34	75.6	949	2 H97322	A; Accession: A01280
17	33	73.3	303	2 T2658	A; Residues: 1-427 <MIN>
18	33	73.3	332	2 T01483	R; Mindruo, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
19	33	73.3	469	2 F69403	J. Biol. Chem. 263, 16051-16054, 1988
20	33	73.3	603	2 S70849	A; Title: A new kinin moiety in human plasma kininogens.
21	33	73.3	706	2 D84466	A; Reference number: A31905; MUID:88209021; PMID:3182782
22	33	73.3	895	2 T23191	A; Accession: A27900
23	32	71.1	484	2 A0774	A; Residues: 381-389 <MAX>
24	32	71.1	562	2 AF0852	R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
25	32	71.1	563	2 S54420	Biochem. Biophys. Res. Commun. 150, 511-516, 1988
26	32	71.1	567	2 E91095	A; Title: Identification of [hydroxyproline(3)-1-lysyl-bradykinin in ascitic f
27	32	71.1	567	2 A85941	A; Reference number: A34030; MUID:88106632; PMID:3337729
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29	32	71.1	1215	2 T25078	A; Molecule type: protein

ALIGNMENTS

Title:	US-09-461-061a-1	KGHNLL
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Sequence:	1 NNATFVFK 8	N; Alternative names: alpha-2-thiol proteinase inhibitor; preprokininogen
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Gapop:	10.0	C; Species: Homo sapiens (man)
Gapext:	0.5	C; Date: 06-Jul-1982 #sequence revision 27-Nov-1985 #text_change 08-Dec-2000
searched:	283224 seqs, 96134422 residues	R; Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Total number of hits satisfying chosen parameters:	283224	J. Biol. Chem. 260, 8601-8609, 1985
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Maximum DB seq length:	2000000000	A; Reference number: A92544; MUID:85234582; PMID:2989293
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	3: Pir3;*	R; Takagaki, Y.; Kitamura, N.; Nakaniishi, S.
	4: Pir4;*	Biochemistry 23, 5691-5697, 1984
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
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		Biochemistry 23, 5691-5697, 1984
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R; Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.; J. Biol. Chem. 260, 8610-8617, 1985
 A; Title: Structural organization of the human kininogen gene and a model for its evolution
 A; Content: annotation; gene organization
 R; Pierce, J.V.
 A; Reference number: A52454; PMID:2989294

A; Cross-references: GDB:KNG; OMIM:228960
 A; Map position: 3q27-3q27
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Query Match 100.0%
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RESULTS 2
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 R; Ohkubo, T.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
 Biochemistry 23, 561-567, 1994
 A; Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its identification
 A; Reference number: A90490; PMID:85122621; PMID:8441591
 A; Accession: A01279
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 R; Takagaki, Y.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A; Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight kininogens
 A; Reference number: A92544; PMID:85234582; PMID:2989293

FEBS Lett. 321, 93-97, 1993
 A; Title: Cloning, expression and characterization of human kininogen domain 3.
 A; Reference number: S32422; PMID:9322385; PMID:8467916
 A; Accession: S32422
 A; Molecule type: mRNA
 A; Residues: ANSM' 253-377 <AVED>
 A; Note: differences are due to known cloning artifacts
 R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A; Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen
 A; Reference number: A91153; PMID:86030270; PMID:4054110
 A; Accession: A91153
 A; Molecule type: protein
 A; Residues: 379-644 <LOT>
 A; Note: the bradykinin sequence preceding the light chain sequence was not determined
 R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A; Title: Completion of the primary structure of human high-molecular-mass kininogen
 A; Reference number: A24871
 A; Accession: A24871
 A; Molecule type: protein
 A; Residues: 2' 20-380 <KEKL>
 R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
 In Kinins IV, Grenebaum, L.M., and Margoliash, H.S., ed., pp. 85-89. Plenum Press, New York, 1986
 A; Title: Amino acid sequence of the light chain of human high molecular mass kininogen
 A; Reference number: A27899
 A; Accession: A27899
 A; Molecule type: protein
 A; Residues: 379-389 'K' 390-407 'Q' 409-644 <KEKL>
 R; Mindruoi, T.; Carretero, O.A.; Proust, D.; Walz, D.; Scicli, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A; Title: A new kinin moiety in human plasma kininogens
 A; Reference number: A27659; PMID:31820901; PMID:31865237
 A; Accession: A27659
 A; Molecule type: protein
 A; Residues: 380-389 <MIN>
 R; Maeda, H.; Matsunaga, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A; Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic fluid
 A; Reference number: A31905; PMID:89034061; PMID:3182782
 A; Accession: A31905
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 R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A; Title: Identification of [hydroxyproline(3)]-1-sylyl-bradykinin released from human platelets
 A; Reference number: A34030; PMID:88106632; PMID:3337729
 A; Accession: A34030
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 R; Leharcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIS) in inflammatory diseases
 A; Reference number: S02462; PMID:89076517; PMID:3264507
 A; Accession: S02482
 A; Molecule type: protein
 A; Residues: 1-19;189-192,310-314,381-389 <LEN1>
 R; Kato, H.; Matsunaga, Y.; Maeda, H.
 FEBS Lett. 232, 252-254, 1988
 A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in human platelets
 A; Reference number: A61495; PMID:88211869; PMID:3366244
 A; Accession: A61495
 A; Molecule type: protein
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R;Lenarcic, B.; Krasovce, M.; Ritonja, A.; Olafsson, I.; Turk, V.

A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.

A;Reference number: S14303; PMID:2013314

A;Molecule type: protein

A;Residues: 264-359,'N',361-375 <LEN2>

R;Little, S.S.; Johnson, D.A.

A;Title: Human mast cell trypsinase isoforms: separation and examination of substrate-specific

A;Reference number: S55239; PMID:7733867

A;Molecule type: protein

A;Residues: 450-452,'X',454,'X',456 <LEN>

R;Straczek, J.; Mauchi, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabert, P.; Belleville

A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like

A;Reference number: S68059; PMID:7589467

A;Molecule type: protein

A;Residues: 431-434 <STP>

R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.

J. Biol. Chem. 260, 8610-8617, 1985

A;Title: Structural organization of the human kininogen gene and a model for its evolution

A;Reference number: A92445; PMID:85234583; PMID:2989294

A;Contents: annotation; gene organization

R;Pierce, J.V.

Fed. Proc. 27, 52-57, 1968

A;Title: Structural features of plasma kinins and kininogens.

A;Reference number: A91455; PMID:90255622; PMID:4952632

A;Contents: annotation; bradykinin

C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene

C;Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the

C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Genetics: Cysteine residue is present in the kininogen prior to the release of bradykinin.

A;Gene: GDB:KNG

A;Cross-references: GDB:125256; OMIM:228960

A;Map position: 3q17-3q17

A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

A;Superfamily: kininogen; cystatin homology

C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl

F:1-18/Domain: signal sequence #status experimental <SIG>

F:1-18/Domain: HMW kininogen I (prokininogen) #status experimental <MAT1>

F:1-18/Domain: HMW kininogen II #status experimental <MAT2>

F:1-18/Domain: HMW kininogen heavy chain #status experimental <RCH>

F:19-379/Domain: HMW kininogen heavy chain #status experimental <CY1>

F:19-131/Domain: cystatin homology <CY2>

F:24-375/Domain: cystatin homology <CY3>

F:24-389/Domain: cystatin homology <CY4>

F:24-389/Domain: lysyl-bradykinin (kallikrein II) #status experimental <KBDY>

F:381-389/Domain: bradykinin (kallikrein I) #status experimental <BDY>

F:390-644/Domain: HMW kininogen light chain #status experimental <LCH>

F:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats

F:431-434/Product: low molecular weight growth-promoting factor #status experimental <GP>

F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F:28-614,63-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/disulfide bonds:

F:48/Binding site: carbohydrate (Asn) (covalent) #status absent

F:169-205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:319-380/Cleavage site: Met-Lys (kallikrein) #status experimental

F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental

F:401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status ex

F:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 45; DB 1; Length 644;

Best Local Similarity 100.0%; Pred. No. 0.52;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

Db 293 NNATFYFK 300

RESULT 3

A;Residues: 380-389 <KAT3>

R;Lenarcic, B.; Krasovce, M.; Ritonja, A.; Olafsson, I.; Turk, V.

A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.

A;Reference number: S14303; PMID:91192133; PMID:2013314

A;Molecule type: protein

A;Residues: 264-359,'N',361-375 <LEN2>

R;Little, S.S.; Johnson, D.A.

A;Title: Human mast cell trypsinase isoforms: separation and examination of substrate-specific

A;Reference number: S55239; PMID:7733867

A;Molecule type: protein

A;Residues: 450-452,'X',454,'X',456 <LEN>

R;Straczek, J.; Mauchi, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabert, P.; Belleville

A;Title: Structural organization of the human kininogen gene and a model for its evolution

A;Reference number: A92445; PMID:85234583; PMID:2989294

A;Contents: annotation; gene organization

R;Pierce, J.V.

Fed. Proc. 27, 52-57, 1968

A;Title: Structural features of plasma kinins and kininogens.

A;Reference number: A91455; PMID:90255622; PMID:4952632

A;Contents: annotation; bradykinin

C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene

C;Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the

C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Genetics: Cysteine residue is present in the kininogen prior to the release of bradykinin.

A;Gene: GDB:KNG

A;Cross-references: GDB:125256; OMIM:228960

A;Map position: 3q17-3q17

A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

A;Superfamily: kininogen; cystatin homology

C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl

F:1-18/Domain: signal sequence #status experimental <SIG>

F:1-18/Domain: HMW kininogen I (prokininogen) #status experimental <MAT1>

F:1-18/Domain: HMW kininogen II #status experimental <MAT2>

F:1-18/Domain: HMW kininogen heavy chain #status experimental <RCH>

F:19-379/Domain: HMW kininogen heavy chain #status experimental <CY1>

F:19-131/Domain: cystatin homology <CY2>

F:24-375/Domain: cystatin homology <CY3>

F:24-389/Domain: cystatin homology <CY4>

F:24-389/Domain: lysyl-bradykinin (kallikrein II) #status experimental <KBDY>

F:381-389/Domain: bradykinin (kallikrein I) #status experimental <BDY>

F:390-644/Domain: HMW kininogen light chain #status experimental <LCH>

F:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats

F:431-434/Product: low molecular weight growth-promoting factor #status experimental <GP>

F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F:28-614,63-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/disulfide bonds:

F:48/Binding site: carbohydrate (Asn) (covalent) #status absent

F:169-205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:319-380/Cleavage site: Met-Lys (kallikrein) #status experimental

F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental

F:401,533,542,546,557,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status ex

F:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 45; DB 1; Length 644;

Best Local Similarity 100.0%; Pred. No. 0.52;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

Db 293 NNATFYFK 300

RESULT 4

A;Residues: 380-389 <KAT3>

R;Lenarcic, B.; Krasovce, M.; Ritonja, A.; Olafsson, I.; Turk, V.

A;Title: Inactivation of human cystatin C and kininogen by human cathepsin D.

A;Reference number: S14303; PMID:91192133; PMID:2013314

A;Molecule type: protein

A;Residues: 264-359,'N',361-375 <LEN2>

R;Little, S.S.; Johnson, D.A.

A;Title: Human mast cell trypsinase isoforms: separation and examination of substrate-specific

A;Reference number: S55239; PMID:7733867

A;Molecule type: protein

A;Residues: 450-452,'X',454,'X',456 <LEN>

R;Straczek, J.; Mauchi, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabert, P.; Belleville

A;Title: Structural organization of the human kininogen gene and a model for its evolution

A;Reference number: A92445; PMID:85234583; PMID:2989294

A;Contents: annotation; gene organization

R;Pierce, J.V.

Fed. Proc. 27, 52-57, 1968

A;Title: Structural features of plasma kinins and kininogens.

A;Reference number: A91455; PMID:90255622; PMID:4952632

A;Contents: annotation; bradykinin

C;Comment: The HMW kininogen precursor and the LMW form are produced from the same gene

C;Comment: Kininogen is a cysteine protease inhibitor, takes part in initiation of the

C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is impo

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i

C;Genetics: Cysteine residue is present in the kininogen prior to the release of bradykinin.

A;Gene: GDB:KNG

A;Cross-references: GDB:125256; OMIM:228960

A;Map position: 3q17-3q17

A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

A;Superfamily: kininogen; cystatin homology

C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl

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F:1-18/Domain: HMW kininogen II #status experimental <MAT2>

F:1-18/Domain: HMW kininogen heavy chain #status experimental <RCH>

F:19-379/Domain: cystatin homology <CY1>

F:19-131/Domain: cystatin homology <CY2>

F:24-375/Domain: cystatin homology <CY3>

F:24-389/Domain: cystatin homology <CY4>

F:24-389/Domain: lysyl-bradykinin (kallikrein II) #status experimental <KBDY>

F:381-389/Domain: bradykinin (kallikrein I) #status experimental <BDY>

F:390-644/Domain: HMW kininogen light chain #status experimental <LCH>

F:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats

F:431-434/Product: low molecular weight growth-promoting factor #status experimental <GP>

F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen

F:28-614,63-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/disulfide bonds:

F:48/Binding site: carbohydrate (Asn) (covalent) #status absent

F:169-205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:319-380/Cleavage site: Met-Lys (kallikrein) #status experimental

F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental

F:401,533,542,546,557,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status ex

F:577/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 100.0%; Score 45; DB 1; Length 644;

Best Local Similarity 100.0%; Pred. No. 0.52;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8

Db 293 NNATFYFK 300

A;Residues: 380-389 <KAT3>

R;Lenarcic, B.; Krasovce, M.; Ritonja, A.; Olafsson, I.; Turk, V.

A;Title: Inactivation of human cystatin C and kininogen (Norway rat)

A;Reference number: S1447

A;Molecule type: protein

A;Residues: 264-359,'N',361-375 <LEN2>

R;Biochem. J. 307, 207-211, 1995

A;Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like

A;Reference number: A92447; PMID:90255622

A;Contents: annotation; gene organization

R;Biochem. J. 307, 207-211, 1995

A;Title: Human mast cell trypsinase isoforms: separation and examination of substrate-specific

A;Reference number: Z19836
A;Accession: T24062
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:1-858 <WILD>
A;Experimental source: clone R09AB.2
A;Gene: CESP:R09AB.2
A;Map Position: X
A;Introns: 197/1; 324/3; 377/3; 435/3; 495/3; 587/1; 627/3; 730/3; 812/1
Query Match 80.0%; Score 36; DB 2; Length 858;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNATFYFK 8
Db 49 NGATFYFK 56

RESULT 6
T31107
telomerase reverse transcriptase - Oxytricha trifallax
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000
C;Accession: T31107
R;Iryan, T.M.; Spenger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95: 8479-8484; 1998
A;Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha
A;Accession number: 220985; PMID:9671703
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1132

A;Cross-references: EMBL:AF060230; NID:93342795; PID:g3342796; PID:93342795; PID:g3342796; PID:93342795
A;Gene: TERT
Query Match 80.0%; Score 36; DB 2; Length 1132;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NNATFYFK 8
Db 1001 NNISFYFK 1008

RESULT 7
T24206
hypothetical protein R12H7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T24206
R;Coles, L.
submitted to the EMBL Data Library, August 1995
A;Reference number: 219854
A;Accession number: T24206
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:250755; PID:CAA90635.1; GSPDB:GN00028; CESP:R12H7.
A;Experimental source: clone R12H7
C;Genetics:
A;Gene: CESP:R12H7.3
A;Map Position: X
A;Introns: 150/3
C;Superfamily: human S-phase kinase-associated protein 1A
Query Match 77.8%; Score 35; DB 2; Length 182;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYFK 8
Db 161 NNATFYFK 168

RESULT 8
B83803
hypothetical protein BH1226 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B83803
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28: 4317-4331; 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:2051258; PMID:11058132
A;Accession: B83803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <STOP>
A;Cross-references: GB:AP001511; GB:BA000004; NID:910173727; PIDN:BAB04945.1; GSPDB:G
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1226

Query Match 75.6%; Score 34; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFYF 7
Db 43 NATFYF 48

RESULT 9
T06978
ABA-induced plasma membrane protein PM 19 - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999
C;Accession: T06978
R;Kolke, M.; Takezawa, D.; Arkawa, K.; Yoshiida, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: T06978
A;Accession: T06978
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-182 <RNA>
A;Cross-references: EMBL:U80037; NID:91724111; PID:g1724111; PID:91724112
A;Experimental source: cv. Chihoku
C;Genetics:
A;Note: WTABAPM

Query Match 75.5%; Score 34; DB 2; Length 182;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7
Db 47 NGATFYF 53

RESULT 10
F86924
hypothetical protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F86924
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroy
d, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002

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Db 238 NNATFYF 244
A;Accession: F86924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <STO>
A;Cross-references: GB:AL450380; NID:913092504; PIDN:CAC29634.1; GSPDB:GN00147
C;Genetics: AL0126

RESULT 13
G9611
probable cytochrome P450 t8f23.21 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G96611
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, M.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, M.; Chung, M.K.; Choi, B.; Huizar, L.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luers, J.S.; Maiti, R.; Marzila, R.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venturi, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <STO>
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <STO>
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Status: preliminary
A;Map position: 1
A;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
C;Genetics:

Db 20 NNAQFYF 26
Query Match 75.6%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 NNAQFYF 26
Query Match 75.6%; Score 34; DB 2; Length 273;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
A86650
rhamnosyltransferase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: A86650
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarrie, K.; Weissbach, J.; Ehrlund, A.; Reference number: A86625; PMID:21235186; PMID:11337471
A;Accession: A86650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <STO>
A;Cross-references: GB:AE005176; PID:912723056; PIDN:AAK04299.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: rgsB

Db 20 NNAQFYF 26
Query Match 75.6%; Score 34; DB 2; Length 319;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 20 NNAQFYF 26
Query Match 75.6%; Score 34; DB 2; Length 319;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12
T11319
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Pedinomonas minor mitochondrion
C;Species: mitochondrion Pedinomonas minor
C;Accession: T11319
R;Turmel, M.; Lemieux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W.
submitted to the EMBL Data Library, December 1998
A;Description: The complete mitochondrial DNA sequences of Nephroelmis olivacea and Pedinomonas minor.
A;Reference number: 217261
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Cross-references: EMBL:AF116775; PIDN:94378766; PIDN:AA19671.1
C;Genetics:
A;Gene: nad2
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion; NADH dehydrogenase (ubiquinone) chain 2; NADH oxidoreductase

Db 80 NNADFYF 86
Query Match 75.6%; Score 34; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 80 NNADFYF 86
Query Match 75.6%; Score 34; DB 2; Length 440;
Best Local Similarity 85.7%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
G9611
probable cytochrome P450 t8f23.21 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G96611
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, M.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, M.; Chung, M.K.; Choi, B.; Huizar, L.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luers, J.S.; Maiti, R.; Marzila, R.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venturi, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <STO>
A;Cross-references: GB:AE005173; NID:911055848; PIDN:ANG28316.1; GSPDB:GN00141
A;Accession: G96611
A;Status: preliminary
A;Map position: 1
A;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
C;Genetics:

Db 64 NNATFYFK 70
Query Match 75.6%; Score 34; DB 2; Length 497;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 64 NNATFYFK 70
Query Match 75.6%; Score 34; DB 2; Length 497;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 14
T25330
hypothetical protein M01A10_4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25830
R;Scheet, P.
submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid M01A10.
A;Reference number: Z20094
A;Accession: T25830
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-630 <SCH>
A;Cross-references: EMBL:U88174; PIDN:ABA42276.1; GSPDB:GN00019; CESP:M01A10.4
A;Experimental source: strain Bristol N2; clone M01A10
C;Genetics:
A;Gene: CESP:M01A10_4
A;Map position: 1
A;Introns: 10/2; 249/3; 284/1

Db 64 NNATFYFK 70
Query Match 75.6%; Score 34; DB 2; Length 630;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 64 NNATFYFK 70
Query Match 75.6%; Score 34; DB 2; Length 630;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
T31944
hypothetical protein C49D10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31994
R;Hankhaus, J.; Wohldmann, P.; Beck, C.
submitted to the EMBL data library, July 1997
A;Description: The sequence of *C. elegans* cosmid C49D10.
A;Reference number: Z21108
A;Accession: T31994
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-758 <HEND>
A;Cross-references: EMBL:AF016665; PIDN: AAC71186.1; GSPDB:GN00020; CESP:C49D10.1
A;Experimental source: strain Bristol N2; clone C49D10
C;Genetics:
A;Gene: CESP:C49D10.1
A;MAP position: 2
A;Introns: 438/2

Query Match Score 34; DB 2; Length 758;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	NNATFYK	8
:	1	1 1	
Db	598	SNAQFYFK	605

Search completed: March 13, 2003, 19:14:01
Job time : 12 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:10:02 ; Search time 5 Seconds
(without alignments)
66.362 Million cell updates/sec

Title: US-09-461-061A-1
Perfect score: 45
Sequence: 1 NNATFYFK 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	45	100.0	644	1	KNG_HUMAN	P01042 homo sapien
2	39	86.7	639	1	KNG_RAT	P08934 rattus norv
3	36	80.0	1132	1	TERT_OXYTR	076332 oxytetracyc
4	33	73.3	603	1	CHLE_MOUSE	Q03311 mus musculus
5	32	71.1	562	1	INVG_SALTY	P35672 salmonella
6	32	71.1	606	1	NU5M_PIG	O70711 sus scrofa
7	32	71.1	1590	1	GCN2_YEAST	P15442 saccharomyces
8	31	68.9	82	1	U2AG_PIG	Q29350 sus scrofa
9	31	68.9	196	1	HIS5_BUCAI	P57204 buchnera ap
10	31	68.9	239	1	U2AG_MOUSE	Q94883 mus musculus
11	31	68.9	240	1	U2AG_HUMAN	Q10181 homo sapien
12	31	68.9	264	1	U2AG_DROME	Q94335 drosophila
13	31	68.9	334	1	ARGC_ECOLI	I14146 escherichia
14	31	68.9	341	1	OMPU_VTBCH	P97085 vibrio chol
15	31	68.9	434	1	KNL2_BOVIN	P11047 bos taurus
16	31	68.9	441	1	PAFA_HUMAN	Q13093 human platelet
17	31	68.9	444	1	PAFA_CANFA	Q28862 canis familiaris
18	31	68.9	619	1	NUC2_BOVIN	P01045 bovis taurinus
19	31	68.9	623	1	RSD1_YEAST	P32368 saccharomyces
20	31	68.9	901	1	VEF_GYPU	P41723 pseudalatium
21	31	68.9	901	1	VEF_GVHN	P29998 trichoplusia
22	31	68.9	902	1	VEF_GVHA	P54432 heliothis a
23	31	68.9	988	1	ST23_YEAST	Q06010 saccharomyces
24	31	68.9	1066	1	NUC2_NEOCR	Q01317 neurospora
25	31	68.9	2710	1	TOXA_CLODI	P16154 clostridium
26	31	68.9	4725	1	DYHC_DICDI	P34036 dictyostellum
27	30	66.7	163	1	SFAS_ECOLI	P34330 escherichia
28	30	66.7	196	1	HIS5_METJUA	Q57329 methanococcus
29	30	66.7	208	1	LEUD_BUCDN	Q85073 buchnera ap
30	30	66.7	237	1	YS76_GAEEL	Q93619 caenorhabditis
31	30	66.7	251	1	Y456_MYCPO	Q99gb0 mycoplasma
32	30	66.7	259	1	KKA6_ACIBA	P09685 acinetobacter
33	30	66.7	259	1	NIXA_HELPJ	Q2zm4 helicobacte

ALIGNMENTS

RESULT 1						
KNG_HUMAN	ID	KNG_HUMAN	STANDARD;	PRT;	644 AA.	
P01042; P01043;	AC					
21-JUL-1986 (Rel. 01, Created)	DT					
01-FEB-1996 (Rel. 33, Last sequence update)	DT					
16-Oct-2001 (Rel. 40, Last annotation update)	DT					
Kininogen Precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Bradykinin].	DE					
KNG.	GN					
Homo sapiens (Human).	OS					
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	OC					
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC					
NCBI_TAXID=9606;	OX					
[1]	RN					
SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).	RP					
TISSUE=Liver;	RC					
MEIDLINE=05234582; PubMed=2989293;	RX					
Takagaki Y., Kitamura N., Nakaniishi S.; Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight prekininogens. Primary structures of two human prekininogens. ".	RA					
"Structural organization of the human kininogen gene and a model for its evolution.".	RA					
J. Biol. Chem. 260:8601-8609(1985).	RL					
[2]	RN					
GENE STRUCTURE.	RP					
MEIDLINE=05234583; PubMed=2989294;	RX					
Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakaniishi S.;	RA					
"Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen.".	RA					
Biochemistry 23:5691-5697(1984).	RL					
[3]	RN					
SEQUENCE OF 1-401 FROM N.A.	RP					
MEIDLINE=05122621; PubMed=6441591;	RX					
Okubo I., Kurachi K., Takasawa T., Shiokawa H., Sasaki M.;	RA					
"Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen.".	RT					
Eur. J. Biochem. 152:307-314(1985).	RL					
[4]	RN					
SEQUENCE OF 379-644.	RP					
MEIDLINE=06030200; PubMed=4054110;	RX					
Lortspeich F., Kellermann J., Henschien A., Foertsch B., Mueller-Esterl W.;	RA					
"The amino acid sequence of the light chain of human high-molecular-mass kininogen."	RA					
Eur. J. Biochem. 152:307-314(1985).	RL					
[5]	RN					
SEQUENCE OF 381-389.	RP					
MEIDLINE=90255622; PubMed=495632;	RX					
Pierce J.V.;" Structural features of plasma kinins and kininogens. "	RA					
Eur. J. Biochem. 27:52-57(1966).	RL					
[6]	RN					
DISULFIDE BONDS.	RP					
Sueyoshi T., Miyata T., Kato H., Iwanaga S.;" Disulfide bonds in bovine HMW kininogens. "	RA					
"Disulfide bonds in bovine HMW kininogens. "	RT					

Seikagaku 56:808-808(1984).
 -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
 HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
 HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
 FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN AND PLASMIN-
 INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
 BRAODYKININ THAT IS RELEASED FROM HMW KININOGEN SHOWS A VARIETY OF
 PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
 CONTRACTION; (4B) INDUCTION OF HYPOTENSION; (4C) NATRIURESES AND
 DIURESES; (4D) DECREASE IN BLOOD GLUCOSE LEVEL; (4E) IT IS A
 MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
 PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
 OTHER MEDIATORS OF INFLAMMATION (E.G. PROTAGLANDINS); (4F) IT HAS
 A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRAODYKININ ACTION); (5)
 INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION; (5)
 LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) HMW-
 KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
 CLOTTING.
 -1- SUBCELLULAR LOCATION: Secreted.
 -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE
 PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- PMID: BRAODYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
 -1- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.

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 or send an email to license@isb-sib.ch).

CC

DR EMBL; K02566; ABB35497.1; .
 DR EMBL; M11431; ABB59550.1; .
 DR EMBL; M11438; ABB59550.1; JOINED.
 DR EMBL; M11521; ABB59550.1; JOINED.
 DR EMBL; M11522; ABB59550.1; JOINED.
 DR EMBL; M11533; ABB59550.1; JOINED.
 DR EMBL; K02566; ABB35497.1; .
 DR EMBL; M11431; ABB59550.1; .
 DR EMBL; M11438; ABB59550.1; JOINED.
 DR EMBL; M11521; ABB59550.1; JOINED.
 DR EMBL; M11522; ABB59550.1; JOINED.
 DR EMBL; M11533; ABB59550.1; JOINED.
 DR EMBL; M11524; ABB59550.1; JOINED.
 DR EMBL; M11525; ABB59550.1; JOINED.
 DR EMBL; M11536; ABB59550.1; JOINED.
 DR EMBL; M11521; ABB59550.1; JOINED.
 DR EMBL; M11528; ABB59550.1; JOINED.
 DR EMBL; M11437; ABB59551.1; .
 DR EMBL; M11438; ABB59551.1; JOINED.
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 DR EMBL; M11521; ABB59551.1; JOINED.
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 DR EMBL; M11525; ABB59551.1; JOINED.
 DR EMBL; M11536; ABB59551.1; JOINED.
 DR PIR; A01280; KGHUH1.
 DR PIR; A01280; KGHL1.
 DR PIR; B25276; B25276.
 DR PIR; S02482; S02482.
 DR SWISS-2DPAGE; P01042; HUMAN.
 DR Genew; HGNC; 6383; KNG.
 DR MIM; 228960; .
 DR InterPro; IPR000010; Cystatin.
 DR Pfam; PF00031; cystatin_3.
 DR PRINTS; PR00334; KININOGEN.
 DR SMART; SM0043; CI_3.
 DR PROSITE; PS00287; CYSTATIN_2.
 KW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
 KW Bradykinin; Blood coagulation; Inflammatory response; Signal;
 KW Alternative splicing.
 FT SIGNAL_1 18
 CHAIN 19 644 KININOGEN.

RL	Seikagaku 56:808-808(1984). -1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN AND PLASMIN- INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRAODYKININ THAT IS RELEASED FROM HMW KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION; (4B) INDUCTION OF HYPOTENSION; (4C) NATRIURESES AND DIURESES; (4D) DECREASE IN BLOOD GLUCOSE LEVEL; (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROTAGLANDINS); (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRAODYKININ ACTION); (5) INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION; (5) LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) HMW- KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD CLOTTING. -1- SUBCELLULAR LOCATION: Secreted. -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.	CC	CHAIN	19	380	KININOGEN HEAVY CHAIN.
		FT	PEPTIDE	381	389	BRAODYKININ.
		FT	CHAIN	390	644	KININOGEN LIGHT CHAIN.
		FT	DOMAIN	19	136	CYSTATIN-LIKE 1.
		FT	DOMAIN	137	258	CYSTATIN-LIKE 2.
		FT	DOMAIN	259	380	CYSTATIN-LIKE 3.
		FT	DOMAIN	420	510	HIS-RICH (ASSOCIATED WITH CLOTTING ACTIVITY).
		FT	REPEAT	420	449	
		FT	REPEAT	450	479	
		FT	REPEAT	480	510	PYRROLIDONE CARBOXYLIC ACID.
		FT	MOD_RES	19	19	INTERCHAIN.
		FT	DISULFID	28	614	
		FT	DISULFID	83	94	
		FT	DISULFID	107	126	
		FT	DISULFID	142	145	
		FT	DISULFID	206	218	
		FT	DISULFID	229	248	
		FT	DISULFID	264	267	
		FT	DISULFID	328	340	
		FT	DISULFID	351	370	
		FT	CARBONYD	48	48	N-LINKED (GLCNAC. . .) (POTENTIAL).
		FT	CARBONYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
		FT	CARBONYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
		FT	CARBONYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
		FT	CARBONYD	401	401	O-LINKED.
		FT	CARBONYD	533	533	O-LINKED.
		FT	CARBONYD	542	542	O-LINKED.
		FT	CARBONYD	546	546	O-LINKED.
		FT	CARBONYD	557	557	O-LINKED.
		FT	CARBONYD	571	571	O-LINKED.
		FT	CARBONYD	577	577	O-LINKED.
		FT	CARBONYD	593	593	O-LINKED.
		FT	CARBONYD	628	628	O-LINKED.
		FT	VARSPLIC	402	427	VSPHHSWAPADEERDSKGEGHTR -> SHLRSCEYKGR PPKGAGPASERES (IN ISOFORM LMW).
		FT	VARSPLIC	428	644	MISSING (IN ISOFORM LMW).
		FT	CONFLICT	593	593	T -> I (IN RF 1).
		SQ	SEQUENCE	644 AA;	71945 MW;	313284CBABFBEE CRC64;
		Query	1 NNATFFYFK 8	100.0%	Score 45; DB 1; Length 644;	
		Db	293 NNATFFYFK 300	100.0%	Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;	
		RESULT	2			
		KNG_RAT	STANDARD			
		ID	P08934; P08933;			
		AC	P08934; P08933;			
		DT	01-NOV-1988 (Rel. 09, Created)			
		DR	01-NOV-1988 (Rel. 09, Last sequence update)			
		DT	16-OCT-2001 (Rel. 40, Last annotation update)			
		DE	Kininogen precursor [Contains: Bradykinin].			
		GN	Rattus norvegicus (Rat).			
		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
		OX	NCBI_TaxID=10116;			
		RN	[1]			
		RP	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).			
		RX	MEDLINE=87137443; PubMed=3029068;			
		RA	Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;			
		RT	"Differing expression patterns and evolution of the rat kininogen gene family";			
		RL	J. Biol. Chem. 262:2190-2198(1987).			
		RN	[2]			
		RP	SEQUENCE FROM N.A. (LMW ISOFORM).			
		RX	MEDLINE=86008264; PubMed=2413018;			
		RA	Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;			

"Primary structures of the mRNAs encoding the rat precursors for bradykinin and t-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor"; J. Biol. Chem. 260:12054-12059 (1985).

[3] SEQUENCE OF 1-65 FROM N.A.
STRAIN-WISTER; TISSUE-Liver;
SPAIN-BUFFALO;
MEDLINE=87250580; PubMed=2439509;

Fung W.P., Schreiber G.;
"Structure and expression of the genes for major acute phase alpha 1-protein (thiostatin) and kininogen in the rat." J. Biol. Chem. 262:9298-9308(1987).

[4] SEQUENCE OF 1-41 FROM N.A.
STRAIN-WISTER; TISSUE-Liver;
Kagayama R., Kitamura N., Ohkubo H., Nakaniishi S.;
"Differing utilization of homologous transcription initiation sites of rat K and T kininogen genes under inflammation condition." J. Biol. Chem. 262:2345-2351 (1987).

-1- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKAJIREKIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (B) INDUCTION OF HYPOTENSION, (C) Natriuresis and diuresis, (D) DECREASE IN BLOOD GLUCOSE LEVEL; (4E) IT IS A MEDiator OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS); (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELIUM DERIVED RELAXING FACTOR ACTION); (5) LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-KININOGEN IS IN CONTRAST TO HMW KININOGEN NOT INVOLVED IN BLOOD

- CLOTHING.
- SUBCELLULAR LOCATION: secreted.
- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPlicing.
- TISSUE SPECIFICITY: PLASMA.
- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
- MISCELLANEOUS: RAT EXPRESS FOR TYPES OF KININOGENS: THE CLASSICAL HMW/LMW KININOGENS AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I AND T-II.
- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.

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(or send an email to license@isdb.sib.ac.cn).

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EMBL: L29428; AAA41486.1; -
EMBL: M11884; AAA41487.1; -
EMBL: M14369; AAA41488.1; -
EMBL: M14369; AAA41485.1; ALT_SEQ.
EMBL: M16455; AAA41482.1; -
PIR: A25486; A25486.
PIR: A28055; A28055.
InterPro: IPR00010; Cystatin.
InterPro: IPR02395; Kininogen.
Pfam: PF00031; cystatin; 3.
PRINTS: PR0034; KININOGEN.
SMART: SM0043; CY; 3.
PROSITE: PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Biotin kinase; Blood coagulation; Inflammatory response; Signal;
Alternative splicing; Multigene family.
SICGNV

```

卷之三

FT	CHAIN	19	639	KININOPEN.
FT	CHAIN	19	380	KININOPEN. HEAVY CHAIN.
FT	PEPTIDE	381	389	BRADYKININ.
FT-	CHAIN	390	639	KININOPEN LIGHT CHAIN.
FT-	DOMAIN	19	136	CYSSTATIN-LIKE 1.
FT	DOMAIN	137	258	CYSSTATIN-LIKE 2.
FT	DOMAIN	259	380	CYSSTATIN-LIKE 3.
FT	DISULFID	439	514	HIS-RICH.
FT	DISULFID	28	609	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	83	94	BY SIMILARITY.
FT	DISULFID	107	126	BY SIMILARITY.
FT	DISULFID	142	145	BY SIMILARITY.
FT	DISULFID	206	218	BY SIMILARITY.
FT	DISULFID	229	248	BY SIMILARITY.
FT	DISULFID	264	267	BY SIMILARITY.
FT	DISULFID	328	340	BY SIMILARITY.
FT	DISULFID	351	370	BY SIMILARITY.
FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	127	127	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	529	529	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	402	433	VSPSKLARQEERDQNEQGPISGHGNWHAQK -> RLLNS
FT	VARSPLIC	434	639	CEVYGRLLKGAGAAGPAPERQEAASVVTP (IN ISOFORM
FT	CONFFLICT	61	61	LAWN).
FT	SEQUENCE	639 AA;	70933 MW;	MISSING (IN ISOFORM LMN).
FT	SEQUENCE	7;	Conservative	E -> K (IN REF. 2).
Qy	1	NNATFYFK	8	Score 39; DB 1; Length 639;
Qy	1	NNHHTFYFK	300	Best Local Similarity 87.5%; Pred. No. 3.7;
Matches	0;	Mismatches	1;	Indels 0; Gaps
Db	293	NNHHTFYFK	300	
RESULT 3				
TERT-OXYTR STANDARD; PRT; 1132 AA.				
AC	078332;			
AC	078332;			
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, Last sequence update)		
DT	30-MAY-2000	(Rel. 39, Last annotation update)		
DE	Telomerase reverse transcriptase (EC 2.7.7.-)	(Telomerase catalytic subunit) (Telomerase subunit P133).		
GN	TERT.			
OS	Oxytricha trifallax.			
OC	Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;			
OC	Stichotrichida; Oxytrichidae; Oxytricha.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Medline-98337940; PubMed=9671703;			
RA	Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;			
RT	"Telomerase reverse transcriptase genes identified in tetrabryphena thermophila and Oxytricha trifallax".			
RT	Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484 (1998).			
CC	-1- FUNCTION: TELOMERASE IS A RIBONUCLEOPROTEIN ENZYME ESSENTIAL FOR THE REPLICATION OF CHROMOSOME TERMINI IN MOST EUKARYOTES. IT ELONGATES TELOMERES. IT IS A REVERSE TRANSCRIPTASE THAT ADDS SIMPLE SEQUENCE REPEATS TO CHROMOSOME ENDS BY COPYING A TEMPLATE SEQUENCE WITHIN THE RNA COMPONENT OF THE ENZYME.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- SIMILARITY: BELONGS TO THE REVERSE TRANSCRIPTASE FAMILY. TELOMERASE SUBFAMILY.			
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CC EMBL; AF06230; AAC39163.1; -.

DR InterPro; IPR00545; Telomerase_RT.

DR PRINTS; PRO01365; TELOMERASERT.

KW DNA-binding; RNA-directed DNA polymerase; Telomerase; Nuclear protein;

KW DNA-binding.

SQ SEQUENCE 1132 AA; 134124 MW; 81E145FFF24392DC CRC64;

Query Match 80.0%; Score 36; DB 1; Length 1132;

Best Local Similarity 75.0%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NNATFFK 8

DB 1001 NNISFFK 1008

RESULT 4

CHLE_MOUSE STANDARD; PRT; 603 AA.

AC Q03311;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Cholinesterase precursor (EC 3.1.1.8) (Acetylcholine acylhydrolase)

(Choline esterase II) (Butyrylcholine esterase)

DE (Pseudocholinesterase).

GN OS Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[1] RN NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.

RX MEDLINE=90380428; PubMed=2400605;

RA Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;

RA "Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternatively spliced mRNA species." / Neuron 5:317-327(1990).

[2] RN SEQUENCE OF 97-237 FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=91201348; PubMed=2016308;

RA Arpagos M., Chattonnet A., Masson P., Newton M., Vaughan T.A.,

RA Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;

RA "Use of the polymerase chain reaction for homology probing of butyrylcholinesterase from several vertebrates." /

RL J. Biol. Chem. 266:5966-5974(1991).

CC - CATALYTIC ACTIVITY: An acetylcholine + H₂O = choline + a carboxylic acid anion.

CC - SUBUNIT: HOMOTRIMER. THE TRIMER IS COMPOSED OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND.

CC - TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES). - MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH ORGANOPHOSPHATE ESTERS.

CC - SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

CC -

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CC EMBL; M99492; AAA37328.1; -.

DR PIR; A39768; A39768.

DR HSSP; P21836; IMAH.

DR MGD; MGI:894275; Bche.

DR InterPro; IPR002018; CarbesteraseB.

DR InterPro; IPR00997; Cholinesterase.

DR IPR00379; Ser_estr_site.

DR PF00135; Coesterase_1.

DR PRINTS; PRO0878; CHOLINESTERASE.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

KW Hydrolase; Serine esterase; Glycoprotein; Signal.

FT SIGNAL 1 29

FT CHAIN 30 603 CHOLINESTERASE.

FT ACT_SITE 227 227 BY SIMILARITY.

FT ACT_SITE 354 354 BY SIMILARITY.

FT ACT_SITE 467 467 BY SIMILARITY.

FT DISULFID 94 121 BY SIMILARITY.

FT DISULFID 281 292 BY SIMILARITY.

FT DISULFID 429 548 BY SIMILARITY.

FT DISULFID 600 600 INTERCHAIN_BY_SIMILARITY.

FT CARBOHYD 86 86 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 135 135 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 270 270 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 370 370 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 484 484 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 510 510 (GLCNAC. . .) (POENTIAL).

FT CARBOHYD 515 515 (GLCNAC. . .) (POENTIAL).

FT CONFLICT 129 129 R > P (IN REF. 2).

SQ SEQUENCE 603 AA; 68521 MW; 71981B220D1E55367 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 603;

Best Local Similarity 85.7%; Pred. No. 48; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 6; Sequence STRAIN=N.TML; PRT; 562 AA.

RESULT 5 INVG_SALTY STANDARD; PRT; 562 AA.

ID INVG_SALTY AC P35672

ID INVG_SALTY AC P35672

ID INVG_SALTY AC P35672

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Invg Protein Precursor.

GN INVG OR SPM2898

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI_TaxID=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N.TML; PRT; 562 AA.

RX MEDLINE=95122719; PubMed=866845;

RA Lodge J., Douce G.R., Amin I.I., Bolton A.J., Martin G.D.,

RA Chatfield S., Dougan G., Brown N.L., Stephen J.J.;

RA "The *Salmonella* typhimurium invasion genes *invF* and *invG* encode homologues of the *Arac* and *PulD* family of proteins." /

RT Mol. Microbiol. 13:555-568(1994).

RL Infec. Immun. 63:762-765(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SR-11; PRT; 562 AA.

RX MEDLINE=9089692; PubMed=7997169;

RA Kaniga K., Bossio J.C., Galan J.E.;

RA "The *Salmonella* typhimurium invasion genes *invF* and *invG* encode

homologues of the *Arac* and *PulD* family of proteins." /

RT Mol. Microbiol. 13:555-568(1994).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=LTC-1 / SGSC1412 / ATCC 700720;

RX MEDLINE=2153498; PubMed=1167769;

RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J.J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,

RA	Waterson R., Wilson R.K.,	Complete genome sequence of <i>Salmonella enterica</i> serovar <i>Typhimurium</i>	RL Gene 236:107-114(1999);	NADH + ubiquinone = NAD(+) + ubiquinol.
RT	L12."		-i - CATALYTIC ACTIVITY:	
RT	Nature 413:852-856(2001).		CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	-1- FUNCTION: INVOLVED IN THE INVASION OF THE CELLS OF THE INTESTINAL		CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	EPITHELIUM. COULD BE NECESSARY FOR THE EXPORT OF INVASION RELATED		CC the European Bioinformatics Institute. There are no restrictions on its	
CC	DETERMINANTS.		CC use by non-profit institutions as long as its content is in no way	
CC	-i - SUBCELLULAR LOCATION: Outer membrane (Potential).		CC modified and this statement is not removed. Usage by and for commercial	
CC	-i - SIMILARITY: BELONGS TO THE PULD/OUTD/EXED/XPSD FAMILY.		CC entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC			CC or send an email to license@isb-sib.ch).	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		CC	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		CC	
CC	or send an email to license@isb-sib.ch).		CC	
DR	X753049; CAR53049_1;		Query Match	71.1%; Score 32; DB 1; Length 606;
EMBL	U08280; AA74040_1;		Best Local Similarity	62.5%; Pred. No. 75;
EMBL	AB008832; AAL21778_1;		Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DR	S38422; S38422;		Qy 1 NNATFYFK 8	
DR	StyGene SG1018B; InvG.		Db 505 NNNTYIYK 512	
DR	InterPro; IPR04846; GPII/IIIprotein.			
DR	InterPro; IPR004845; GPIIproteinC.			
PFam	PF00263; GPII_III;			
DR	PROSITE; PS00875; T2SP_D; 1.			
DR	Virulence; Transport; Protein transport; Signal; Outer membrane;			
KW	Complete proteome.			
FT	SIGNAL 1 14 POTENTIAL.		RESULT 7	
FT	CHAIN 15 562 INGV PROTEIN.		GCN2_YEAST	
FT	CONFLICT 12 12 A -> R (IN REF. 2).		ID GCN2_YEAST	
FT	CONFLICT 121 121 E -> Q (IN REF. 2).		AC P15442;	
FT	CONFLICT 197 205 LRIQQMVF -> CAIRKWLFR (IN REF. 2).		DT 01-APR-1990 (Rel. 14, Created)	
FT	CONFLICT 232 240 ANPAFSAANG -> RCQOFORM (IN REF. 2).		DT 01-NOV-1991 (Rel. 20, Last sequence update)	
FT	CONFLICT 243 243 G -> S (IN REF. 2).		DT 30-MAY-2000 (Rel. 39, Last annotation update)	
FT	CONFLICT 262 264 AAA -> KPAEQ (IN REF. 2).		DE Protein kinase GCN2 (EC 2.7.1.-).	
FT	CONFLICT 328 328 S -> T (IN REF. 1 AND 2).		GN GCN2 OR AACI OR YDR28C.	
FT	CONFLICT 329 329 I -> V (IN REF. 2).		OS Saccharomyces cerevisiae (Baker's yeast).	
FT	CONFLICT 370 380 RPVLLTQINVP -> APITSSSKCS (IN REF. 2).		OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces.	
SEQUENCE	562 AA; 61765 MW; 8022905BE256058D CRC64;		OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
RN	[1]		OX NCBI_TAXID=4932;	
RP	SEQUENCE FROM N.A.		RN [1]	
RX	MEDLINE-89282814; PubMed=2660141;		RX SEQUENCE FROM N.A.	
RA	Wek R.C., Jackson B.M., Hinnebusch A.G.;		RX MEDLINE-89282814; PubMed=2660141;	
RT	"Juxtaposition of domains homologous to protein kinases and histidyl-		RA Roussou I., Thireos G., Hagine B.M.;	
RT	tRNA synthetases in GCN2 protein suggests a mechanism for coupling		RT transcriptional-translational regulatory circuit in <i>Saccharomyces</i> and the	
RT	GCN4 expression to amino acid availability.";		RT GCN2 protein kinase;"	
RT	Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).		RL Mol. Cell. Biol. 8:2132-2139(1988).	
RN	[2]		RN [3]	
RP	SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.	
RC	STRAIN=288C;		RC STRAIN=288C;	
RX	MEDLINE-88261291; PubMed=3280651;		RX MEDLINE-88261291; PubMed=3280651;	
RA	Roussou I., Thireos G., Hagine B.M.;		RA Roussou I., Thireos G., Hagine B.M.;	
RT	"Ribosome association of GCN2 protein kinase, a translational		RT Ribosome association of GCN2 protein kinase, a translational	
RT	cerevisiae which involves the GCN4 transcriptional activator and the		RT activator of the GCN4 gene of <i>Saccharomyces cerevisiae</i> ."	
RT	GCN2 protein kinase;"		RT	
RT	Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).		RL Mol. Cell. Biol. 8:2132-2139(1988).	
RN	[4]		RN [5]	
RP	ASSOCIATION WITH RIBOSOMES.		RP ASSOCIATION WITH RIBOSOMES.	
RX	MEDLINE-91246169; PubMed=2038314;		RX MEDLINE-91246169; PubMed=2038314;	
RA	Ramirez M., Wek R.C., Hinnebusch A.G.;		RA Ramirez M., Wek R.C., Hinnebusch A.G.;	
RT	"Ribosome association of GCN2 protein kinase, a translational		RT activator of the GCN4 gene of <i>Saccharomyces cerevisiae</i> ."	
RT	activator of the GCN4 gene of <i>Saccharomyces cerevisiae</i> ."		RT	
RT	Proc. Natl. Acad. Sci. U.S.A. 86:4579-4583(1989).		RL Mol. Cell. Biol. 8:2132-2139(1988).	
RA	[5]		RN [5]	
RP	ACTIVITY ON SUI2.		RP ACTIVITY ON SUI2.	
RX	MEDLINE-92154672; PubMed=1739968;		RX MEDLINE-92154672; PubMed=1739968;	

RA Dever T.E., Feng L., Wek R.C., Cigan A.M., Donahue T.D.,
 RA Hinnebusch A.G.; Cigan A.M., Donahue T.D.,
 RA "Phosphorylation of initiation factor 2 alpha by protein kinase GCN2
 mediates gene-specific translational control of GCN4 in yeast.";
 RR Cell 68: 585-596(1992).
 I- FUNCTION: STIMULATES GCN4 TRANSLATION IN AMINO ACID-STARVED CELLS
 CC BY PHOSPHORYLATING THE ALPHA SUBUNIT OF EIF-2 (SUI2) ON SER-52.
 CC -I- SUBCELLULAR LOCATION: ASSOCIATES WITH THE 60S SUBUNIT OF
 CC RIBOSOMES.
 CC -I- INDUCTION: BY AMINO ACID STARVATION AND IN THE PRESENCE OF THE
 CC GCNA PROTEIN.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC GCN2 SUBFAMILY.
 CC -I- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 301
 CC TO 364 AND FROM POSITION 981 ONWARD DUE TO FRAMESHIFTS.
 CC
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 CC
 DR M27082; AAA34636_1;
 DR EMBL; U51030; ABB64461_1; ALT_FRAME.
 DR PIR; M20487; AAA34881_1; ALT_INIT.
 DR SGD; S0002691; GCN2.
 DR InterPro; IPR002106; AACRNA_ligaseII.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_pkr_pkinase.
 DR Pfam; PF0069; pkinase; 3.
 DR PROSITE; PS50862; AA_tRNA_LIGASE_II; FALSE_NEG.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
 RW Amino-acid_transf erase; Serine/threonine-protein kinase; ATP-binding;
 FT DOMAIN 187 458 PROTEIN_KINASE_1.
 FT DOMAIN 530 912 PROTEIN_KINASE_2.
 FT DOMAIN 930 1450 HISTIDYL-TRNA_SYNTHETASE LIKE.
 FT NP_BIND 536 544 ATP (BY SIMILARITY).
 FT BINDING 559 559 ATP (BY SIMILARITY).
 FT ACT_SITE 766 766 BY SIMILARITY.
 FT CONFLICT 151 157 TIKAKLP->NYGGKIA (IN REF. 2).
 FT CONFLICT 202 210 LMSSERMMEN->YVFSNIGKS (IN REF. 2).
 FT CONFLICT 406 406 I->M (IN REF. 2).
 FT CONFLICT 520 520 P->A (IN REF. 2).
 FT CONFLICT 523 536 RSRYASDFEITAVL->DHDMLLTKLKRHFS
 FT CONFLICT 553 553 (IN REF. 2).
 FT CONFLICT 571 572 S->T (IN REF. 2).
 FT CONFLICT 658 658 IL->MI (IN REF. 2).
 FT CONFLICT 658 658 F->C (IN REF. 2).
 FT CONFLICT 770 770 M->K (IN REF. 2).
 FT CONFLICT 885 885 E->Q (IN REF. 2).
 SQ SEQUENCE 1590 AA; 182041 MW; 768B15424F64FLAA CRC64;

Query Match 71.1%; Score 32; DB 1; Length 1590;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Gaps 0; Indels 0; Gaps 0;

QY 1 NNATYFK 8
 | : ||| : |
 Db 266 NNATFWKK 273

RESULT 8
 U2AG_PIG STANDARD; PRT; 82 AA.

RESULT 9
 ID HISS5_BUCAI STANDARD; PRT; 196 AA.
 AC P57704;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Imidazole_glycerol amidotransferase subunit hish (EC 2.4.2.-) (IGP
 DE synthase glutamine amidotransferase subunit) (IGP synthase subunit
 DE hish) (Igsp synthase subunit hish) (Igsp subunit hish).
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 OS symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID-118099;
 RN [1]

SEQUENCE FROM N.A.

STRAIN=Tokyo 1998; MEDLINE=20445173; PubMed=10993077;

RC RX Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.", RT Nature 407:81-86(2000).

-1- FUNCTION: IGP5 catalyzes the conversion of PREAR and glutamine to IGP, AICAR and glutamate. The hish subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hifse for the synthesis of IGP and AICAR (By similarity).

CC -1- CATALYTIC Activity: 5-[(5-phospho-1-deoxyribulos-1-yiamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5'-carboxylic acid-ribonucleotide + L-glutamate + H(2)O.

CC -1- PATHWAY: Histidine biosynthesis; fifth step.

CC -1- SUBUNIT: Heterodimer of hish and hisf (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.

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CC DR EMBL; AP001118; BAB12822; 1; .

CC DR InterPro; IPRO00991; GATase_1.

CC DR Pfam; PF00117; GATase; 1.

CC FT PROTE; PS00442; GATASE_TYPE_I; FALSE_NEG.

CC KW Histidine biosynthesis; Transferase; Glutamine amidotransferase; Complete proteome.

CC FT ACT_SITE 77 BY SIMILARITY.

CC FT ACT_SITE 178 BY SIMILARITY.

CC FT ACT_SITE 180 BY SIMILARITY.

CC SEQUENCE 196 AA; 21679 MW; 904624B74BBEBE5D CRC64;

Query Match Score 68.9%; Pred. No. 37; DB 1; Length 196;

Best Local Similarity 71.4%; Pred. No. 37; DB 1; Length 196;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATYYF 7

Db 135 NNSREYF 141.

RESULT 10

U2AG_MOUSE STANDARD; PRT; 239 AA.

ID 09D813; Q9CZ98; Q99LX2;

DT 15-JUN-2002 (Rel. 41; Created)

DT 15-JUN-2002 (Rel. 41; Last sequence update)

DE Splicing Factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 snRNP auxiliary factor small subunit).

GN U2AF1.

OS Mus musculus (Mouse); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10030;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21085650; PubMed=11217851;

RA Kawai J., Shigenawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batzler S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nakaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Cartron P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., RA Wynnshaw-Borisi A., Yoshida K., Whittaker C., Wilming L., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.", RT Nature 409:685-690(2001).

RL RN [12]

RP SEQUENCE OF 2-239 FROM N.A.

RC TISSUE=Breast tumor;

RA Strausberg R.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN INTERACTIONS AND PROTEIN-RNA INTERACTIONS REQUIRED FOR ACCURATE 3'-SPlice SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHancers AND THUS MAY FUNCTION AS A BRIDGE BETWEEN U2AF65 AND THE ENHANCER COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON (By similarity).

CC -1- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN (By similarity).

CC -1- DOMAIN: The C-terminal SR-rich domain is required for interactions with SR proteins and the splicing regulators TRA and TRA2, and the N-terminal domain is required for formation of the U2A35/U2AF65 heterodimer (By similarity).

CC -1- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.

CC -1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.

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CC DR EMBL; AK001118; BAB25609; 1; .

CC DR EMBL; BC002184; AAH02184; 1; .

CC DR MGD; MG1:98884; U2af1.

CC DR InterPro; IPR000504; RNA_rec_mot.

CC DR InterPro; IPR003954; RRM_1.

CC DR InterPro; IPR00571; Znf_CCHH.

CC DR Pfam; PF00076; rrm1; 2.

CC DR Pfam; PF00642; zf-CCCH; 4.

CC DR SMART; SM00361; RRM_1; 1.

CC DR SMART; SM00356; Znf_C3H1; 2.

CC DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.

CC KW Nuclear protein, RNP-binding; mRNA splicing; Zinc-finger; Repeat.

FT ZNFING 13 4 1 C3H1-TYPE 1.

FT DOMAIN 65 147 RNA-BINDING (RRM).

FT ZNFING 149 173 C3H1-TYPE 2.

FT DOMAIN 179 238 ARG/GLY/SER-RICH (RS DOMAIN).

FT CONFLICT 187 187 G > R (IN REF. 1; BAB25609).

SQ SEQUENCE 239 AA; 27815 MW; DFF944210581244D CRC64;

Query Match Score 68.9%; Length 239;

Best Local Similarity 71.4%; Pred. No. 46;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NATEYFK 8

Db 17 NCSEYFK 23

RESULT 1.1				
U2AF_HUMAN	STANDARD;	PRT;	240 AA.	
ID U2AC_HUMAN				
AC Q01081; DT 01-APR-1993 (Rel. 25, Created)				
DT 01-APR-1993 (Rel. 25, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
Splicing factor U2AF 35 kDa subunit (U2 auxiliary factor 35 kDa subunit) (U2 snRNP auxiliary factor small subunit).				
DE U2AF1 OR U2AF35.				
GN Homo sapiens (Human).				
EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID=9606;				
OX RN				
SEQUENCE FROM N.A., AND SEQUENCE OF 68-89 AND 126-151.				
RC RX				
TISSUE-Fetal brain; MEDLINE-92409598; PubMed=1388271;				
RA RA				
OHKI M., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillihabel M., Schudy A., Zimmemann W., Rosenthal A., Sasada T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandst P., Scharfe M., Schoen O., Desario C., Kawer G., Bloecker H., Ransier J., Beck A., Klages S., Hennig S., Riesselmann L., Degand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.; "The DNA sequence of human chromosome 21."; Nature 405:311-319(2000). [1]				
RL RN				
SEQUENCE FROM N.A.				
RP RX				
MEDLINE-20283799; PubMed=10830953;				
RA RA				
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillihabel M., Schudy A., Zimmemann W., Rosenthal A., Sasada T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandst P., Scharfe M., Schoen O., Desario C., Kawer G., Bloecker H., Ransier J., Beck A., Klages S., Hennig S., Riesselmann L., Degand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.; "The DNA sequence of human chromosome 21."; Nature 405:311-319(2000). [1]				
RP RP				
FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN INTERACTIONS AND PROTEIN RNA INTERACTIONS REQUIRED FOR ACCURATE 3'-SPLICING SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHancers AND THIS MAY FUNCTION AS A BRIDGE BETWEEN U2AF5 AND THE ENHancer COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON.				
RA RA				
"The splicing factor U2AF35 mediates critical protein-protein interactions in constitutive and enhancer-dependent splicing."; Zuo P., Maniatas T.; "The splicing factor U2AF35 mediates critical protein-protein interactions with the SR protein SRS domain is required for interactions with SR proteins and the splicing regulators TRA and TRB2, and the N-terminal SR-rich domain is required for formation of the U2AF35/U2AF65 heterodimer.				
RT RT				
"The splicing factor U2AF35 mediates critical protein-protein interactions in constitutive and enhancer-dependent splicing.";				
RI CC				
Genes Dev. 10:1366-1368(1996).				
-1- FUNCTION: PLAYS A CRITICAL ROLE IN BOTH CONSTITUTIVE AND ENHANCER-DEPENDENT SPLICING BY MEDIATING ESSENTIAL PROTEIN-PROTEIN INTERACTIONS AND PROTEIN RNA INTERACTIONS REQUIRED FOR ACCURATE 3'-SPLICING SITE SELECTION. DIRECTLY MEDIATES INTERACTIONS BETWEEN U2AF65 (LARGE SUBUNIT) AND PROTEINS BOUND TO THE ENHancers AND THIS MAY FUNCTION AS A BRIDGE BETWEEN U2AF5 AND THE ENHancer COMPLEX TO RECRUIT IT TO THE ADJACENT INTRON.				
CC CC				
"-1- SUBUNIT: ASSOCIATES WITH A 65 kDa PROTEIN.				
CC CC				
"-1- DOMAIN: The C-terminal SR-rich domain is required for interactions with SR proteins and the splicing regulators TRA and TRB2, and the N-terminal domain is required for formation of the U2AF35/U2AF65 heterodimer.				
CC CC				
"-1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).				
CC CC				
"-1- SIMILARITY: CONTAINS 2 C3H1-TYPE ZINC FINGERS.				
CC CC				
"-1- SIMILARITY: BELONGS TO THE SR FAMILY OF SPLICING FACTORS.				
CC CC				
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CC CC				
EMBL; M96982; AAA36619.1; .				
DR DR				
Durbin K.J., Doup L.E., Downe N., Dugov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Feirreira S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
EMBL; AP001748; BAA9534.1; .				

Query Match 68.9%; Score 31; DB 1; Length 334;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFVK 8
Db 109 NDATFVK 116

RESULT 14

OPMU_VIBCH ID OMPU_VIBCH STANDARD; PRT; 341 AA.
AC P97085; Q915A3; Q9KU50;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Outer membrane protein U precursor (Porin ompU).
GN OMPU OR VC0633.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
RN SEQUENCE FROM N.A.
RC STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1;
RX MEDLINE=97101065; PubMed=945536;
RA Speradio V., Bailey C.C., Giron J.A., Dirita V.J., Silveira W.D.,
RA Vettore A.L., Kaper J.B.;
RN "Cloning and characterization of the gene encoding the OmpU outer
membrane protein of Vibrio cholerae.";
RL Infect. Immun. 64:5406-5409(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=EL Tor;
RN Yin Y., Zhang J.Z.;
RN "Cloning and expression of ompU of Vibrio cholerae and its
antigenicity analysis.";
RN Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor NI6961 / Serotype O1;
RX MEDLINE=20040683; PubMed=0959301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Utayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermoljeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RN "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RT Nature 406:477-483(2000).
RN [4]
CC 1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
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DR EMBL; AF253529; AAF4526_1;
DR EMBL; AE004149; AAF3799_1; ALT_INIT.
DR TIGR; VC0633; -.
DR InterPro; IPR031229; OMP_2.
DR Pfam; PF00267; Gram-ve_porins_1.
KW Transmembrane; Porin; Signal; Outer membrane; Complete proteome.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 341 OUTER MEMBRANE PROTEIN U.
FT CONFLICT 278 278 F -> I (IN REF. 2).
FT CONFLICT 290 290 E -> K (IN REF. 1).

FT CONFLICT 324 341 AA; 325 36645 MW; VG -> AS (IN REF. 1).
SQ Query Match 68.9%; Score 31; DB 1; Length 341;
Best Local Similarity 71.4%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NATFVK 8
Db 299 DATFVK 305

RESULT 15

KNL2_BOVIN ID KNL2_BOVIN STANDARD; PRT; 434 AA.
AC P01047;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Kininogen, LMW II precursor (Thiol proteinase inhibitor) [Contains:
DE Bradykinin].
OS Bos taurus (Bovine).
OC Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
NCBI_TaxID=9131;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=83117859; PubMed=6572010;
RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RA Miyata T., Iwanaga S.;
RA RT Primary structures of bovine liver low molecular weight kininogen
precursors and their two mRNAs."
RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
RN [2]
RN SEQUENCE OF 19-376.
RP MEDLINE=8137530; PubMed=3546295;
RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Miyata T., Iwanaga S.;
RA RT Bovine high molecular weight kininogen. The amino acid sequence,
RT Positions of carbohydrate chains and disulfide bridges in the heavy
RT chain portion."
RL J. Biol. Chem. 262:2768-2779(1987).
CC [-] FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC LMW-KININogen INHIBITS THE AGGREGATION OF THROMBOCYTES; (3) THE
CC ACTIVE PEPTIDE PHYSIOLOGICAL EFFECTS: (3A) INFLUENCE IN SMOOTH
CC MUSCLE CONTRACTION. (3B) INDUCTION OF HYPOtENSION,
CC Natriuresis and diuresis (KIDNEY).
CC [-] SUBCELLULAR LOCATION: Extracellular.
CC [-] ALTERNATIVE PRODUCTS: 2 isoforms; LMW II (shown here) and HMW II
CC (AC P01045); are produced by alternative splicing.
CC [-] TISSUE SPECIFICITY: PLASMA.
CC [-] PTM: BRADYKININ IS RELEASED FROM KININogen BY PLASMA KALLIKREIN.
CC [-] MISCELLANEOUS: LMW-KININogen IS IN CONTRAST TO HMW-KININogen NOT
CC INVOLVED IN BLOOD CLOTTING.
CC [-] SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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CC [-]
DR EMBL; V00427; CAA23710_1; -.
DR PIR; A01284; KGB02.
DR HSSP; P01038; 1A90.
DR InterPro; IPR00010; Cystatin.
DR Pfam; PF00031; cystatin; 3.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS0287; CYSTATIN; 2.
DR Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

KW	Thiol protease inhibitor;	Bradykinin;	Signal.
FT	SIGNAL	1	18
FT	CHAIN	19	434
FT	CHAIN	19	KININOGEN, LMW II.
FT	PEPTIDE	378	376
FT	CHAIN	386	HEAVY CHAIN.
FT	BRADYKININ.		
FT	LIGHT CHAIN.		
FT	DOMAIN	19	CYSPTAIN-LIKE 1.
FT	DOMAIN	136	CYSPTAIN-LIKE 2.
FT	DOMAIN	257	CYSPTAIN-LIKE 3.
FT	MOD. RES	19	PYRROLIDONE CARBOXYLIC ACID.
FT	CARBOHYD	87	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	136	O-LINKED (PARTIAL). . .).
FT	CARBOHYD	168	N-LINKED (GLCNAC. . .); OR 169.
FT	CARBOHYD	197	N-LINKED (GLCNAC. . .) (PARTIAL).
FT	CARBOHYD	204	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	280	N-LINKED (GLCNAC. . .).
FT	DISULFID	27	INTERCHAIN.
FT	DISULFID	404	
FT	DISULFID	82	
FT	DISULFID	93	
FT	DISULFID	106	
FT	DISULFID	125	
FT	DISULFID	141	
FT	DISULFID	144	
FT	DISULFID	205	
FT	DISULFID	217	
FT	DISULFID	228	
FT	DISULFID	247	
FT	DISULFID	261	
FT	DISULFID	264	
FT	DISULFID	325	
FT	DISULFID	337	
FT	DISULFID	348	
SQ	SEQUENCE	34	AA; 48148 MW; 73A7079DE3E03430 CRC64;

Query Match 68.9%; Score 31; DB 1; Length 434;
 Best Local Similarity 62.5%; Pred. No. 83;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Job time : 6 secs

QY 1 NNATPFYFK 8
 Db 290 HDGTFIFYFK 297

Search completed: March 13, 2003, 19:13:24

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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:27 ; Search time 16.667 Seconds
 (without alignments)

98.903 Million cell updates/sec

Title: US-09-461-061a-1

Perfect score: 45

Sequence: 1 NNATEYFK 8

Scoring table: BLOSUM62

Gapov 10.0 , Gapext 0.5

searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_virus;*
- 16: sp_bacterioplasm;*
- 17: sp_archeap;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	36	80.0	858	5	Q21853	Q21853 caenorhabdi
2	35	77.8	182	5	Q21968	Q21968 caenorhabdi
3	35	77.8	628	16	Q8R147	Q8R147 fusobacteri
4	34	75.6	71	16	Q9KD17	Q9KD17 bacillus ha
5	34	75.6	115	15	Q9XXT3	Q9XXT3 human immun
6	34	75.6	173	10	Q9ZRF8	Q9ZRF8 oryza sativ
7	34	75.6	181	10	Q9M625	Q9M625 hordeum vul
8	34	75.6	182	10	P93615	P93615 triticum ae
9	34	75.6	273	16	Q9CD90	Q9CD90 mycobacteri
10	34	75.6	326	12	Q66771	Q66771 equine rota
11	34	75.6	326	12	Q66771	Q66771 equine rota
12	34	75.6	326	12	Q66771	Q66771 equine rota
13	34	75.6	326	12	Q91887	Q91887 human rotav
14	34	75.6	357	13	Q91655	Q91655 xenopus lae
15	34	75.6	440	8	Q9ZYV3	Q9ZYV3 pedionomous
16	34	75.6	497	10	Q9FVFS9	Q9FVFS9 arabiopsis

ALIGNMENTS

RESULT	1	Q21853	PRELIMINARY;	PRT;	858 AA.
ID	Q21853				
AC	Q21853;				
DT	01-NOV-1996	(TREMBL1. 01, Created)			
DT	01-NOV-1996	(TREMBL1. 01, Last sequence update)			
DT	01-DEC-2001	(TREMBL1. 19, Last annotation update)			
DE	R09AB..2.	protein.			
GN	R09AB..2.				
OS	Caenorhabditis elegans,				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;				
OX	NCBI_TaxID=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	WILKINSON J.J.				
RL	Submitted (NOV-1995)				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	WILKINSON J.J.				
RA	None;				
RT	"Genome sequence of the nematode C.elegans: A platform for investigating biology."				
RT	Investigating biology."/				
RL	Science 282:2012-2018 (1998).				
DR	EMBL: 268009; CAA92004..1..				
SQ	SEQUENCE 858 AA;	96262 MN;	60E1070CA8F4D4C8 CRC64;		
Query Match	80 0%	Score 36;	DB 5;	Length 858;	
Best Local Similarity	75.0%	Pred. No. 95;			
Matches	6;	Conservative 1; Mismatches 1;	Indels 0;	Gaps 0;	
Qy	1 NNATPFYKF 8				
	:				
Db	49 NESTFYFK 56				

RESULT 2

Q21968 PRELIMINARY; PRT; 182 AA.

ID Q22649

RESULT 4
 AC Q21968; PRELIMINARY; PRT; 71 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE R12H7.3 protein.
 GN R12H7.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peledorinae; Caenorhabditis.
 OX NCBI_TAXID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Submitted (AUG-1995) to the EMBL/GenBank/DDJBJ databases
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99099613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology";
 RL Science 282:2012 (2018:1998).
 DR InterPro: IPR001232; Skp1.
 DR Pfam: PF01466; Skp1; 1.
 DR SMART: SM00512; Skp1; 1.
 SQ SEQUENCE 182 AA; 21178 MW; 4BE36A19C4FA8124 CRC64;
 Query Match 77.8%; Score 35; DB 5; Length 182;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
 QY 1 NNATFYFK 8
 DB 161 NNATFYFK 168

RESULT 4
 Q9KDI7 PRELIMINARY; PRT; 71 AA.
 ID Q9KDI7
 AC Q9KDI7; PRELIMINARY; PRT; 71 AA.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE R12H7.3 protein.
 GN R12H7.3.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TAXID=866665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512589; PubMed=11058132;
 RA Takami H.; Nakatone K.; Takaki Y.; Maeno G.; Sasaki R.; Masui N.;
 RA Fuji F.; Hirama C.; Nakamura Y.; Ogasawara N.; Kuwara S.;
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis* .";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR AP001511; BAB0945; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 71 AA; 8026 MW; 311AC9AE3C539D3 CRC64;

Query Match 75.6%; Score 34; DB 16; Length 71;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NATFYF 7
 DB 43 NATFYF 48

RESULT 5
 Q9YXT3 PRELIMINARY; PRT; 115 AA.
 ID Q9YXT3
 AC Q9YXT3; PRELIMINARY; PRT; 115 AA.
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE Envelope glycoprotein C2V3 region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TAXID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R0596BRP071;
 RA Tanuri A.; Swanson P.A.; Devre S.G.; Berro O.J.; Sayedra A.';
 RA Costa L.J.; Brindeiro R.; Schable C.; Pieniazek D.;
 RA Rayfield M.;
 RA "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil. .";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR AF034019; AAC9271; 1.
 DR InterPro: IPR000777; GPI20.
 DR Pfam: PF00516; GPI20; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON-TER 1
 SQ SEQUENCE 115 AA; 12755 MW; 6551LE67B32DCP56C CRC64;

Query Match 75.6%; Score 34; DB 15; Length 115;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNATFYFK 8
 DB 1111:1:
 DR 78 NNNTFFER 85

RESULT 6				
Q9ZRF8	PRELIMINARY;	PRT;	173 AA.	
ID Q9ZRF8;				
AC 09ZRF8;				
DT 01-MAY-1999 (TREMBLrel. 10, Created)				
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE Hydrophobic LEA-like protein.				
OS Oryza sativa (Rice).				
OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC Triticeae; Triticum.				
NCBI_TAXID=4565;				
RN [1]				
SEQUENCE FROM N.A.				
RC STRAIN=LOMELLO;				
RA Chen L.J., Chai Y.J., Chen P.W.;				
RT "A rice embryo-specific gene with high homology to soybean GmPM3 gene,				
RT a hydrophobic LEA protein gene."				
RT Submitted (May-1996) to the EMBL/GenBank/DBJ databases.				
RL EMBL; U57639; AAD10377.1;				
DR U57639; AAD10377.1;				
SQ SEQUENCE 173 AA; 1827 MW; 63FA2F78BB7259D CRC64;				
Query Match 75.6%; Score 34; DB 10; Length 173;				
Best Local Similarity 85.7%; Pred. No. 50;				
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
RESULT 9				
Q9CD90	PRELIMINARY;	PRT;	273 AA.	
ID Q9CD90;				
AC Q9CD90;				
DT 01-JUN-2001 (TREMBLrel. 17, Created)				
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)				
DE Hypothetical protein ML0126.				
GN GN0126.				
OS Mycobacterium leprae.				
OC Bacteria; Firmicutes; Actinobacteria; Actinomycetidae;				
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
NCBI_TAXID=1789;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=TN;				
RX MEDLINE=2.1/28732; PubMed=11234002;				
RA Cole S.T., Elgjelle K., Parrill J., James K.D., Thomson N.R.,				
RA Wheeler P.R., Garnier T., Churcher C., Harris D.,				
RA Mundall K., Basham D., Brown D., Chillingworth T., Connor R.,				
RA Holroyd S., Devlin K., Dutchoy S., Feltwell T., Fraser A., Hamlin N.,				
RA Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,				
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,				
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,				
RA Stevens K., Taylor K., Woodward J.R., Whitehead S., Barrell B.G.;				
RA "Massive gene decay in the leprosy bacillus.";				
RT RL Nature 409:1007-1011(2001);				
DR DR EMBL; AL583917; CAC29634.1; -.				
SQ SEQUENCE 273 AA; 3081 MW;				
Query Match 75.6%; Score 34; DB 16; Length 273;				
Best Local Similarity 85.7%; Pred. No. 77;				
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
RESULT 8				
P93615	PRELIMINARY;	PRT;	182 AA.	
ID P93615;				
AC P93615;				
DT 01-MAY-1997 (TREMBLrel. 03, Created)				
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE ABA-induced plasma membrane protein PM 19.				
GN WTABA_P.				
OS Triticum aestivum (Wheat).				

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Rhamnosyltransferase.
GN RGDB OR LL0201.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacilli; Clostridium group; Lactobacillales.
OC Streptococcaceae; Lactococcus.
OX NCBI_TAXID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LL1403;
RX MEDLINE=2125186; PubMed=11337471;
RA Bolotin A., Winkel P., Mauger S., Jaillon O., Malarme K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis LL1403.";
RT Genome Res. 11:731-753(2001);
DR EMBL: AE006258; AAK04299.1; -.
HSSP; P39621; 106Q.
DR InterPro; IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Transferase; Complete proteome.
SEQUENCE 319 AA; 37340 MW; D1DCT7BAB0A950CA CRC64;

Query Match 75.6%; Score 34; DB 16; Length 319;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Caps 0;

Qy 1 NNATFYF 7
Db 80 NNADFYF 86

RESULT 11
ID Q66771; PRELIMINARY; PRT; 326 AA.
AC Q66771;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Glycoprotein VP7.
OS Equine rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus
NCBI_TAXID=10937;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR8;
RX MEDLINE=95113988; PubMed=7814511;
RA Clarlet M., Reggetti F., Pina C.I., Liprandi F.;
RT "Equine rotaviruses with G14 serotype specificity circulate among
venezuelan horses.";
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FR8; PubMed=7814511;
RA Clarlet M., Reggetti F., Pina C.I., Liprandi F.;
RT "Equine rotaviruses with G14 serotype specificity circulate among
venezuelan horses.";
RN [1]
RP SEQUENCE FROM N.A.
RC U05349; AAA67342.1; -.
DR InterPro; IPR001963; VP7.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
SQ SEQUENCE 326 AA; 37352 MW; 9095B64B13933E29 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYF 8
Db 318 NSATFYR 325

RESULT 13
ID Q91EB7; PRELIMINARY; PRT; 326 AA.
AC Q91EB7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Capsid protein.
GN VP7.
OS Human rotavirus.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TAXID=10941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC425;
RA Griffin D.D., Nakagomi T., Hoshino Y., Nakagomi O., Kirkwood C.D.,
Parashar U.D., Glass R.I., Gentsch J.R.;
RT "Characterization of non-typeable rotavirus strains from the United
States: Identification of a new rotavirus reassortant (P2A[6],G12) and
rare P3[9] strains related to bovine rotaviruses.";
RT Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR AJ311738; CAC3312.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF00434; VP7; 1.
DR ProDom; PD000191; VP7; 1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
SQ SEQUENCE 326 AA; 37119 MW; 8B97ED1DBBD1C981 CRC64;

Query Match 75.6%; Score 34; DB 12; Length 326;
Best Local Similarity 62.5%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNATFYF 8
Db 318 NSATFYR 325

RESULT 14
ID Q91655; PRELIMINARY; PRT; 357 AA.
AC Q91655;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Gene 17 protein.

RESULT 12
ID Q66772; PRELIMINARY; PRT; 326 AA.
AC Q66772;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

Search completed: March 13, 2003, 19:13:02
 Job time : 18.667 secs

GN GENE 17. Xenopus laevis (African clawed frog). PubMed=8700866;
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TAXID=3355;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96312514; PubMed=8700866;
 RA Brown D.D., Wang Z., Furlow J.D., Kanamori A., Schwartzman R.A.,
 Remo B.F., Pinder A.;
 RT "The thyroid hormone-induced tail resorption program during Xenopus
 laevis metamorphosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
 EMBL; U41860; AAC59876.1;
 DR InterPro; IPR001507; Endoglin/CD105.
 PFAM; PF00100; zona_pellucida_1.
 SMART; SM00241; ZP; 1.
 DR SMART; SM00241; ZP; 1.
 SQ SEQUENCE 357 AA: 39090 MW: 5493352C8EEA21E6 CRC64;

Query Match 75.6%; Score 34; DB 13; Length 357;
 Best Local Similarity 85.7%; Pred. No. 1e-02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7
 ||||| |
 Db 141 NNATLYF 147

RESULT 15

Q9ZY23 PRELIMINARY; PRT; 440 AA.
 ID Q9ZY23;
 AC Q9ZY23;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 2 (EC 1.6.5.3).
 GN NAD2.
 OS Pedinomonas minor.
 OG Eukaryota; Viridiplantae; Chlorophyta; Pedinophyceae; Pedinomonadales;
 OC Pedinomonadaceae; Pedinomonas.
 OC NCBI_TAXID=3159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX LB 1350;
 RX MEDLINE=99418884; PubMed=10488238;
 RA Turmel L.M., Lemieux C., Burger G., Lang B.F., Otis C., Plante I.,
 Gray M.W.;
 RT "The complete mitochondrial DNA sequences of *Nephroselmis olivacea* and
Pedinomonas minor: two radically different evolutionary patterns
 within green algae.";
 RL Plant Cell 11:1717-1729(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UTEX LB 1350;
 RA Burger G.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL: AF116775; ADD19671.1;
 DR InterPro; IPR001750; oxidored_q1.
 PFAM; PF00361; oxidored_q1.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 440 AA; C6D6C9AD72549B4C CRC64;

Query Match 75.6%; Score 34; DB 8; Length 440;
 Best Local Similarity 85.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNATFYF 7
 ||||| |
 Db 238 NNRLFYF 244

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:07:07 ; search time 42 Seconds

(without alignments)

50.762 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATFYFKIDNKKAR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS1/godata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
1	84 100.0	16	21 AAY95410	Anti-angiogenic D3
2	84 100.0	32	21 AAY95408	Anti-angiogenic D3
3	84 100.0	117	14 AAR33350	Domaine 3, bradyki
4	84 100.0	122	21 AAB37447	Human kininogen D3
5	84 100.0	123	21 AAY95426	Human high mol. wt.
6	84 100.0	248	22 ABG21102	Novel human diagno
7	84 100.0	369	22 ABG21099	Human high molecu
8	84 100.0	626	23 ABB75707	Novel human diagno
9	84 100.0	644	22 ABG21101	Novel human high molecu
10	84 100.0	644	23 ABB75710	Composition for inhibiting angiogenesis and endothelial cell

Homo sapiens.

PN WO200035407-A2.

XX

PD 22-JUN-2000.

XX

PR 16-DEC-1998; 980S-0112427.

XX

PF 02-DEC-1999; 99WO-US28465.

XX

PA (UTEM) UNIV TEMPLE.

PA (MCCR) MCCRAE R K.

XX

PI McCrae RK;

XX

DR WPI; 2000-442247/38.

XX

PT Composition for inhibiting angiogenesis and endothelial cell

RESULT 1

AAY95410

standard; Peptide: 16 AA.

ID AAY95410

XX

AC AAY95410;

XX

DT 25-SEP-2000 (first entry)

XX

DE Anti-angiogenic D3 peptide.

XX

KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;

KW rheumatoid arthritis; cytotatic; antiarthritic; antirheumatic;

KW therapy; human; D3 peptide.

XX

OS Homo sapiens.

PN WO200035407-A2.

XX

PD 22-JUN-2000.

XX

PR 16-DEC-1998; 980S-0112427.

XX

PF 02-DEC-1999; 99WO-US28465.

XX

PA (UTEM) UNIV TEMPLE.

PA (MCCR) MCCRAE R K.

XX

PI McCrae RK;

XX

DR WPI; 2000-442247/38.

XX

PT Composition for inhibiting angiogenesis and endothelial cell

ALIGNMENTS

11	78	92.9	18 AAW54336
12	70	83.3	22 ABG21105
13	59	70.2	5 AAP40533
14	57	67.9	21 AAB05553
15	56	66.7	23 ABG60077
16	54	64.3	436 5 AAP40557
17	49	58.3	9 AAB37455
18	45	53.6	10 AAY95409
19	45	53.6	16 AAY95409
20	45	53.6	554 23 ABP27632
21	44	52.4	867 20 AAY34381
22	44	52.4	875 20 AAG32793
23	43	51.2	466 23 ABBA8863
24	41	48.8	872 23 ABF77619
25	41	48.8	996 23 ABH94160
26	40	47.6	74 22 AAO05226
27	40	47.6	152 21 AAG32794
28	40	47.6	153 21 AAG32795
29	40	47.6	166 21 AAG7378
30	40	47.6	179 21 AAY32469
31	40	47.6	1191 22 ABB6075
32	39	46.4	12 21 AAY95407
33	39	46.4	701 21 AAY51007
34	38	45.2	40 23 AAO89365
35	38	45.2	42 22 AAG7378
36	38	45.2	44 23 AAU90167
37	38	45.2	121 21 AY81200
38	38	45.2	128 21 AAY81189
39	38	45.2	156 18 AAW20537
40	38	45.2	222 21 AAB52576
41	38	45.2	277 23 AAG7378
42	38	45.2	282 22 AAG92301
43	38	45.2	316 22 AB62195
44	38	45.2	345 18 AAW20757
45	38	45.2	360 23 ABH92315

PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog -
 XX Claim 7; Page 26; 44pp; English.

CC The present sequence is that of a D3 peptide derived from human
 CC high mol. wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys382.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC inhibiting endothelial cell proliferation, and inducing endothelial
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 CC The IC50 value for the present peptide was less than 0.8 μ M for
 CC inhibition of fibroblast growth factor-induced HUVEC cell
 CC proliferation.
 XX Sequence 16 AA;

Query Match 100.0%; Score 84; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNATFYFKIDNVKKAR 16
 Db 1 NNATFYFKIDNVKKAR 16
 AC AAY95408;

XX 25-SEP-2000 (first entry)
 XX Anti-angiogenic D3 peptide.
 DE XX
 KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytosstatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 XX Homo sapiens.
 OS WO200035407-A2.
 PN XX
 XX 22-JUN-2000.
 PD XX
 PF 02-DEC-1999; 99WO-US28465.
 XX
 PR 16-DEC-1998; 98US-0112427.
 XX
 PA (UTEM) UNIV TEMPLE.
 PA (MCCR) MCCRAE R K.
 PI McCrae RK;
 XX DR; 2000-442247/38.
 XX

XX Composition for inhibiting angiogenesis and endothelial cell
 PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain
 PT 3 analog -
 XX Claim 4; Page 26; 44pp; English.
 XX The present sequence is that of a D3 peptide derived from human

CC high mol. wt. kininogen (HK) domain 3 (see AAY95426). The D3 peptide
 CC inhibits endothelial cell proliferation and thus possesses
 CC anti-angiogenic activity. It is an example of D3 peptides of the
 CC invention (see AAY95405-26) that are analogues of certain sites in
 CC the HK domain 3, in this case amino acid residues Asn275-Lys382.
 CC The peptides inhibit endothelial cell proliferation and may also
 CC induce endothelial cell apoptosis. Compositions including the
 CC peptides are used in claimed methods for inhibiting angiogenesis,
 CC cell apoptosis. Cancer, rheumatoid arthritis, and ocular disorders
 CC characterized by undesired vascularization of the retina are treated.
 XX Sequence 32 AA;

Query Match 100.0%; Score 84; DB 21; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNATFYFKIDNVKKAR 16
 Db 1 NNATFYFKIDNVKKAR 28

RESULT 3
 AAR33350 standard; protein; 117 AA.
 ID AAR33350
 XX
 AC AAR33350;
 XX DT 01-JUL-1993 (first entry)
 DE XX
 DE Domaine 3, bradykinin release activating peptide.
 XX KW Domain 3; human kininogen; heavy chain; low molecular weight; plasma;
 KW trypsin; platelet; activation; granule contents; hemostasis; thrombin;
 KW tissue plasminogen activator; thrombosis; inflammatory response;
 KW endothelial cell; von Willebrand factor;
 XX OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 1..18
 FT /note= "Leader Peptide"
 FT Protein
 FT 19..117 /note= "Nature Protein"
 FT XX
 PN WO9303748-A.
 XX
 PD 04-MAR-1993.
 XX
 PF 13-AUG-1997; 92WO-US066809.
 XX
 PR 13-AUG-1991; 91US-0744545.
 XX
 PA (UTEM) UNIV TEMPLE.
 XX
 PI Jiang Y, Schmaier AB;
 XX DR; 1993-093714/11.
 XX
 PT Use of trypsin-cleavage fragment of human kininogen - for
 PT increasing vascular bradykinin release, for lowering blood
 PT pressure and treating hypertension
 XX
 PS Disclosure; Fig 1; 46pp; English.

XX
 CC The sequence given represents domain 3, amino acids 246-362, of
 CC the human kininogen heavy chain. Domain 3 was isolated from low
 CC molecular weight kininogen, derived from human plasma, by cleavage
 CC with trypsin. Domain 3 peptide inhibits platelet activation
 CC a marked decrease in the platelets ability to aggregate and secrete
 CC their granule contents. The granule contents comprise proteins which
 CC participate in hemostasis, thrombosis and the inflammatory response.

CC Domain 3 also inhibits endothelial cell activation shown by a decrease
 CC in secretion of endothelial cell contents such as tissue plasminogen
 CC activator and von Willebrand factor. Domain 3 functions to inhibit
 CC cell activation by blocking thrombin binding to its target cells, the
 CC peptide is a selective inhibitor of thrombin-induced platelet
 activation.

XX Sequence 117 AA;
 Query Match 100.0%; Score 84; DB 14; Length 117;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 Db 30 NNATFYFKIDNVKKAR 45

RESULT 4
 ID AAB37447 standard; protein; 122 AA.
 XX AAB37447
 AC
 XX 21-FEB-2001 (first entry)
 DT
 XX Human kininogen D3.
 DE
 XX Enzyme; legumain; endopeptidase; cystatin; human; kininogen.
 KW
 XX Homo sapiens.
 OS
 XX WO2006945-A1.
 PN
 XX 02-NOV-2000.
 PD
 XX 20-APR-2000; 2000WO-GB01571.
 PF
 XX 22-APR-1999; 99GB-0009133.
 PR
 XX (BABR-) BABRAHAM INST.
 PA
 XX Abrahamson M, Barrett AJ;
 PI
 XX WPI; 2000-687316/67.
 DR
 XX Inhibition of mammalian legumain or legumain-related endopeptidase by
 PT cystatin involves interaction with second papain-non reactive site of
 PT cystatin.
 PT
 XX Sequence 122 AA;
 PS Disclosure; Fig 4; 45PP; English.

XX The present invention relates to inhibition of the enzymatic activity of
 CC legumain or a legumain related endopeptidase by cystatin. The inhibition
 CC involves an interaction between legumain and a papain-non reactive site
 CC of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and
 CC performs a protein processing function. The present sequence is human
 CC kininogen D3, which was used in the present invention. Kininogen is a
 CC type 3 cystatin.
 XX Sequence 122 AA;

Query Match 100.0%; Score 84; DB 21; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 Db 35 NNATFYFKIDNVKKAR 50

RESULT 5
 AAY95426

ID AAY95426 standard; Peptide; 123 AA.
 XX AAY95426;
 AC
 XX 25-SEP-2000 (first entry)
 DT
 XX Human high mol.wt. kininogen domain 3.
 DE
 XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;
 KW endothelial cell proliferation; apoptosis; cancer; ocular disorder;
 KW rheumatoid arthritis; cytosstatic; antiarthritic; antirheumatic;
 KW therapy; human; D3 peptide.
 OS Homo sapiens.
 XX WO200035407-A2.
 PN
 XX 22-JUN-2000.
 PD
 XX 02-DEC-1999; 99WO-US28465.
 PF
 XX 16-DEC-1998; 98US-0112427.
 PR
 XX (UTEM) UNIV TEMPLE.
 PA
 XX (MCCR/) MCCRAE R K.
 PA
 XX McCrae RK;
 PI
 XX Disclosure; Page 4; 44PP; English.
 DR
 XX The present sequence is that of domain 3 of human high mol.wt.
 CC kininogen (HK). The invention provides peptides (see AAY95405-24)
 CC that are analogues of certain sites in the HK domain 3.
 CC specifically Asn215-Tyr282, Cys246-Cys249, Leu331-Tyr338 and
 CC Tyr339-Ser341. The peptides, in which native Cys residues may be
 CC replaced by Ala residues, inhibit endothelial cell proliferation
 CC and may also induce endothelial cell apoptosis. Compositions
 CC including the peptides are used in claimed methods for inhibiting
 CC angiogenesis, inhibiting endothelial cell proliferation, and
 CC inhibiting endothelial cell apoptosis. Cancer, rheumatoid arthritis,
 CC and ocular disorders characterized by undesired vascularization of
 CC the retina are treated.
 XX Sequence 123 AA;

Query Match 100.0%; Score 84; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OS Homo sapiens.
 Db 41 NNATFYFKIDNVKKAR 56

RESULT 6
 ABG21102
 ID ABG21102 standard; Protein; 248 AA.
 AC
 XX ABG21102;
 DT
 XX 18-FEB-2002 (first entry)
 DE
 XX Novel human diagnostic protein #21093.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PR 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 PA (HYSEQ) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX PI WPI; 2001-639362/73.
 DR N-PSDB; AAS85286.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 PS Claim 20; SEQ ID No 51458; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences, (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (III) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG310377 represent novel human diagnostic amino acid sequences of the invention.
 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 248 AA;
 Query Match Score 84; DB 22; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NNATFYFKIDNVKKAR 16
 | ||| ||| ||| ||| ||| |||
 Db 90 NNATFYFKIDNVKKAR 105
 ! RESULT 8
 ABB75707
 : ID ABB75707 standard; Protein: 626 AA.
 XX AC ABB75707;
 XX DT 18-JUL-2002 (first entry)
 XX DE Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.
 XX KW Human; kininogen; high molecular weight kininogen; HK; D5 domain;
 KW D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;
 KW antiatherosclerotic; vasotropic; transmobiliser; thrombolytic;
 KW ophthalmological; gynaecological; antilulcer; antidiabetic; antiarthritic;
 KW antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
 XX OS Homo sapiens.

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 384..508
 /label= D5_domain
 XX
 WO200214369-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 24-JUL-2001; 2001WO-US23185.
 XX
 PR 24-JUL-2000; 2000US-220194P.
 XX
 PA (ANTE-) ATTENTION LLC.
 XX
 PI Mazar AP, Juarez JC;
 XX
 DR WPI; 2002-393611/4Z.
 XX
 PT Novel human kininogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign hyperplasia -
 XX
 PS Disclosure: Page 13; 84pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kininogen, or biologically active peptide fragment, homologe or functional derivative, and which:
 CC (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required for maintenance of EC viability.
 CC (1) has cytostatic, antitumour, antiatherosclerotic, vasotrope, vulnerary, tranquilliser, thrombolytic, ophthalmological, gynaecological, antilulcer, antidiabetic, antiarthritic, antiangiogenic, antiapoptotic and endocrine activities.
 CC An antibody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide (II) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X) comprising (I), (II), or (III), can be used for treating a subject having a disease or condition associated with undesired EC migration, proliferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the mature human high molecular weight kininogen (HK) protein, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 626 AA;
 Query Match 100.0%; Score 84; DB 23; Length 626;
 Best Local Similarity 100.0%; Pred. No. 8e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNATFYFKIDNVKKAR 16
 DB 275 NNATFYFKIDNVKKAR 290
 RESULT 9
 ABG1101
 ID ABG1101 standard; Protein; 644 AA.
 XX
 AC ABG21101;
 XX
 DT 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #21092.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic;

KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Dermanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS85288.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
 PT
 PT
 PT
 PT
 XX
 PS Claim 20; SEQ ID No 51460; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 84; DB 22; Length 644;
 Best Local Similarity 100.0%; Pred. No. 8.3e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NNATFYFKIDNVKKAR 16
 DB 293 NNATFYFKIDNVKKAR 308
 RESULT 10
 ! RESULT 10
 ABB78710
 ID ABB78710 standard; Protein; 644 AA.
 XX
 AC ABB78710;
 XX
 DT 18-JUL-2002 (first entry)
 DE Human high molecular weight kininogen (HK) protein.
 XX
 KW Human; kininogen; high molecular weight kininogen; HK; D5 domain;
 KW D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;
 KW antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic;

KW ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;
 KW antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.
 XX OS Homo sapiens.

FH Key Peptide
 FT /label= signal
 Protein
 FT /label= mature_human_high_molecular_weight_kininogen
 FT Disulfide-bond 28..614
 FT Disulfide-bond 83..94
 FT Disulfide-bond 107..126
 FT Disulfide-bond 142..145
 FT Disulfide-bond 206..218
 FT Disulfide-bond 229..248
 FT Disulfide-bond 264..267
 FT Disulfide-bond 328..340
 FT Disulfide-bond 351..370
 Domain 402..526
 FT /label= D5_domain
 XX PN WO200214369-A2.
 XX PD 21-FEB-2002.
 XX PP 24-JUL-2001; 2001WO-US23105.
 XX PR 24-JUL-2000; 2000US-220194P.
 XX PA (ATTEN) ATTENON LLC.
 XX PI Mazar AP, Juarez JC;
 XX DR WPI; 2002-393611/42.
 XX Novel human kininogen D5 domain polypeptides useful for treating
 PT conditions associated with endothelial cell migration, proliferation,
 PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign
 PT hyperplasia -
 XX Disclosure: Fig 1B-E; 84PP; English.
 XX The present invention describes an isolated polypeptide (I) that
 CC corresponds to the D5 domain of human kininogen, or biologically active
 CC peptide fragment, homologous or functional derivative, and which:
 CC (a) inhibits angiogenesis; (b) binds to the D5 binding site on
 CC endothelial cells (EC); (c) activates signalling pathways leading to the
 CC introduction of apoptosis in EC; and/or (d) inhibits the signalling
 CC pathway required for maintenance of EC viability. (I) has cytostatic,
 CC antitumour, antithrombotic, vasoconstrictive, tranquilliser,
 CC thrombolytic, opthalmological, antiangiogenic, antiulcer, antidiabetic,
 CC antidiarrhoeal, antiparoxysmal, antiapoptotic and endocrine activities.
 CC An antibody (IX) specific for an epitope of (I) is useful for inhibiting
 CC tumour growth or angiogenesis in a subject. (I), a D5 fusion polypeptide
 CC (II) or a dimeric or trimeric fusion polypeptide (III) can be used for
 CC inhibiting EC migration, proliferation, invasion, or angiogenesis, or
 CC composition (X) comprising (I), (II), or (III), can be used for treating
 CC a subject having a disease or condition associated with undesired EC
 CC migration, proliferation, invasion or angiogenesis. (I), (II), or (III)
 CC can be used for isolating a D5 domain binding molecule from a complex
 CC mixture and for isolating or enriching cells expressing D5 domain binding
 CC sites from a cell mixture. The present sequence represents the human
 CC high molecular weight kininogen (HK) protein, which is given in the
 CC exemplification of the present invention.
 XX Sequence 644 AA;

Query Match 1 NNATFYFKIDNVKKAR 16
 Best Local Similarity 100.0%; Score 84; DB 23; Length 644;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNVKKAR 16
 Db 293 NNATFYFKIDNVKKAR 308

RESULT 11
 AAW54336
 ID AAW54336 standard; peptide; 26 AA.
 XX
 AC AAW54336;
 XX DT 30-JUL-1998 (first entry)
 DE Bradykinin analogous peptide 19.
 XX KW Inhibition: thrombin-induced platelet; prevention; platelet aggregation;
 ADP-induced activation.
 XX OS Synthetic.
 XX PN WO9641640-A1.
 XX PD 27-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US09940.
 XX PR 09-JUN-1995; 95US-0000096.
 XX PA (UNMI) UNIV MICHIGAN.
 XX PI Hasan AAK, Schmaier AH;
 XX DR WPI; 1997-065304/06.
 XX Disclosure: Page 44; 73pp; English.
 XX Inhibition of platelet activation and aggregation - by admin. of new
 PT or known bradykinin analogues
 XX PS Disclosure: Page 44; 73pp; English.
 XX CC Administration of a peptide or multimer related to bradykinin or other
 CC disclsoed peptides and multimers can be used for the inhibition of
 CC thrombin-induced platelets or other cells. They can also be used for
 CC preventing platelet aggregation, or inhibiting ADP-induced activation.
 CC This is useful to prevent arterial occlusions arising from coronary
 CC thrombosis and stroke.
 XX SQ Sequence 26 AA;
 XX Best Local Similarity 92.9%; Score 78; DB 18; Length 26;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NATFYFKIDNVKKAR 16
 Db 1 NATFYFKIDNVKKAR 15

RESULT 12
 ABG21105
 ID ABG21105 standard; protein; 435 AA.
 XX AC ABG21105;
 XX DR 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #21096.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.

XX 11-OCT-2001. PN JP59125896-A.
 XX PD XX 20-JUL-1984.
 XX PF XX 07-JAN-1983; 83JP-0000984.
 XX PR XX 07-JAN-1983; 83JP-0000984.
 PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 XX PA (MITU) MITSUBISHI CHEM IND KK.
 XX DR WPI; 1984-216122/35.
 XX DR N-PSDB; AAN40314.
 DR
 C-Dna fragment of protein precursor - used to code bradykinin
 XX PS Disclosure; Fig 2; 6 pp; Japanese.
 XX CC Bradykinin is a peptide consisting of nine amino acids. It has the
 CC biological effect of decreasing blood pressure. Although kininogen
 CC is known as a protein-precursor of bradykinin, its structure is unknown
 CC because of the difficulty in collecting large enough samples of
 CC kininogen for structural investigation.
 XX Sequence 434 AA;
 SQ Query Match Score 59; DB 5; Length 434;
 Best Local Similarity 73.3%; Pred. No. 0.091;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX QY 1 NNATPFKIDNVKKA 15
 :: ||||| / | | | |
 Db 290 HDGTPFVKIDNVKKA 304
 RESULT 14
 AAB0553 standard; Peptide; 16 AA.
 ID AAB0553 standard; Peptide; 16 AA.
 XX AC AAB0553;
 XX DT 20-DEC-2000 (first entry)
 XX Peptide identified from an origin of prepro-bradykinine.
 DE XX Precursor Peptide; polypeptide hormone; peptide identification.
 KW XX Unidentified.
 OS XX
 XX FH Key
 FT Modified-site 1
 FT Modified-site 16 /note= "hydrogen attached"
 XX FT /note= "amidated residue"
 XX PN WO200050636-A1.
 XX PD 31-AUG-2000.
 XX PF 24-FEB-2000; 2000WO-FR00460.
 AC XX
 XX PR 25-FEB-1999; 99US-0257525.
 DT 30-JUL-1992 (first entry)
 XX PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
 DE PA (CNRS) CNRS CENT NAT RECH SCI.
 XX PI Camara Ferrer YJA, Thirieu C, Martinez J, Berge G, Goze C;
 KW DR
 XX
 XX Location/Qualifiers
 FH 378 .386
 FT 391 ..395
 Key Peptide
 Peptide /label= bradykinin
 Peptide /note= "probe (AAN40241)-encoded sequence"
 FT XX
 FT XX
 FT XX
 FT XX

PS Claim 16; Page 20; 40PP; French.
 XX The specification describes a method for identifying a peptide having a particular function. The method comprises preparing a database of polynucleotides and polypeptides of unknown functions, screening the database for a combination of nucleotides or amino acids indicative of the peptide with a particular function, and identifying polynucleotides and proteins which contain the peptide. The method is used to identify precursor peptides with an amidated C-terminus, especially polypeptide hormones, for studying physiologically active substances. The present sequence represents a peptide which was identified using the method of the invention.

XX Sequence 16 AA:
 Query Match 67.9%; Score 57; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0051%;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YFKIDNVKKAR 16
 Db 1 YFKIDNVKKAR 11
 RESULT 15
 ID ABG60077 standard; Protein: 235 AA.
 XX ABG60077;
 XX DT 30-JUL-2002 (first entry)
 XX DE Human DITHP polypeptide #35.
 XX Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorder; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney; adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen; thymus.
 XX Homo sapiens.
 XX PN WO2002020754-A2.
 XX PD 14-MAR-2002.
 XX PF 29-AUG-2001; 2001WO-US27127.

CC (INCY-) INCYTE GENOMICS INC.
 PA XX
 CC XX
 CC Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
 CC Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
 CC Momiyama MG, Bradley DL, Rohatgi SB, Harris B, Roseberry AM;
 CC Gerstlin EH, Peralta CH, David MH, Panter SR, Flores V, Daffo A;
 CC Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
 XX WEI; 2002-383054/41.
 DR N-PSDB; ABK1668.
 XX PT An isolated polynucleotide useful in diagnostics and therapeutics -
 XX PS Claim 29; Page 610-611; 686PP; English.
 XX PS The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DITHP polypeptides).
 CC The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers (e.g. tumours of the adrenal gland, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus); autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis); viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. ulcerative colitis, lysisuria) and transport disorders (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences ABG59343-ABG60220 represent human DITHP polypeptides of the invention.

SQ Sequence 235 AA;
 Query Match 66.7%; Score 56; DB 23; Length 235;
 Best Local Similarity 73.3%; Pred. No. 0.15;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNATFFKIDNVKKAA 15

Db :||||||| 102 HNHLYFFKIDNVKKAA 116

Search completed: March 13, 2003, 19:12:03
 Job time : 43 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw mode

Run on: March 13, 2003, 19:10:57 ; Search time 15.333 Seconds
(without alignments)
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Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATFYFKIDNVKKAR 16

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	84	100.0	117	1	US-09-193-114B-1	Sequence 1, Appli
2	84	100.0	117	5	PCT-US92-06809-1	Sequence 1, Appli
3	78	92.9	26	4	US-08-076-242-15	Sequence 3, Appli
4	40	47.6	179	3	US-08-911-321-3	Sequence 3, Appli
5	38	45.2	608	1	US-08-66-014-3	Sequence 3, Appli
6	38	45.2	872	1	US-08-166-014-2	Sequence 2, Appli
7	37	44.0	149	4	US-08-679-193A-85	Sequence 85, Appli
8	37	44.0	229	4	US-09-134-201C-3050	Sequence 3050, Appli
9	37	44.0	302	4	US-09-182-205-14	Sequence 14, Appli
10	37	44.0	305	4	US-09-282-205-12	Sequence 12, Appli
11	37	44.0	365	2	US-08-515-251A-2	Sequence 2, Appli
12	36	43.5	514	1	US-08-161-901-21	Sequence 21, Appli
13	36.5	43.5	514	1	US-08-79-919-21	Sequence 21, Appli
14	36.5	43.5	514	1	US-08-483-432-21	Sequence 4, Appli
15	36	42.9	159	4	US-09-030-670C-5	Sequence 5, Appli
16	36	42.9	167	4	US-09-134-001C-3554	Sequence 3554, Appli
17	35.5	42.3	320	1	US-08-126-525-4	Sequence 4, Appli
18	35.5	42.3	320	2	US-08-487-942-4	Sequence 4, Appli
19	35.5	42.3	320	2	US-08-726-036A-4	Sequence 4, Appli
20	35.5	42.3	320	4	US-09-083-516-4	Sequence 4, Appli
21	35.5	42.3	358	1	US-08-153-155A-36	Sequence 8, Appli
22	35.5	42.3	1171	1	US-08-445-135-1	Sequence 1, Appli
23	35	41.7	222	1	US-08-328-152A-8	Sequence 12, Appli
24	35	41.7	240	1	US-07-940-861-12	Sequence 12, Appli
25	35	41.7	240	2	US-08-459-512-12	Sequence 12, Appli
26	35	41.7	240	2	US-08-459-057-12	Sequence 12, Appli
27	35	41.7	240	2	US-08-460-132-12	Sequence 12, Appli

Query Match Score 84; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 1
US-08-193-114B-1
; Sequence 1, Application US/08193114B
; Patent No. 5472945
; GENERAL INFORMATION:
; APPLICANT: Schmaier, Alvin H.
; Jjiang, Yongping
; TITLE OF INVENTION: Modulation of Blood
; Pressure and Inhibition of Platelet Activation
; with Kininogen Fragment
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna &
; Monaco, P.C.
; STREET: 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,114B
; FILING DATE: 9 February 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Application
; APPLICATION NUMBER: Serial No. 5472945 07/744, 545
; FILING DATE: 13 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-137 CII
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3383
; TELEFAX: (215) 568-5549
; TELEX: No. 5472945-e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: peptide
; TOPOLOGY: linear
; US-08-193-114B-1

QY 1 NNATFYFKIDNYKKAR 16
 1|1|1|1|1|1|1|1|1|1|1|
 Db 30 NNATFYFKIDNYKKAR 45

RESULT 2
 PCT-US92-06809-1
 ; Sequence 1, Application PC/TUS9206809
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmaier, Alvin H.
 ; APPLICANT: Jiang, Yongping
 ; TITLE OF INVENTION: Modulation of Blood
 ; TITLE OF INVENTION: Pressure by Altering Bradykinin Levels
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Temple University - Of the
 ; ADDRESS: Commonwealth System of Higher Education
 ; STREET: 406 University Services
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: U.S.A.
 ; ZIP: 19122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/06809
 FILING DATE: 19910813
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Application
 APPLICATION NUMBER: Serial No. 744,545
 FILING DATE: 13 August 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Monaco, Daniel A.
 REGISTRATION NUMBER: 30,480
 REFERENCE/DOCKET NUMBER: 6056-137

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-8833
 TELEFAX: (215) 568-5549

TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear

PCT-US92-06809-1

Query Match Score 84; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNATFYFKIDNYKKAR 16
 1|1|1|1|1|1|1|1|1|1|1|
 Db 30 NNATFYFKIDNYKKAR 45

RESULT 3
 US-08-676-242-15
 ; Sequence 15, Application US/08676242C
 ; Patent No. 6143719
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of Michigan
 ; APPLICANT: Hasan, Ahmed A.K.
 ; TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors
 ; FILE REFERENCE: 8820-2 US
 ; CURRENT APPLICATION NUMBER: US/08/676,242C
 ; CURRENT FILING DATE: 2000-07-16

ORGANISM: Feline herpesvirus-1
 STRAIN: 1
 INDIVIDUAL ISOLATE: C-27
 CELL TYPE: N/A
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD: Deduced sequence
 OTHER INFORMATION: ICP18.5
 US-08-911-321-3

Query Match 47.6%; Score 40; DB 3; Length 179;
 Best Local Similarity 54.5%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNATYFKIDNVV 12
 Db 21 NTAYFFSVENV 31

RESULT 5
 Sequence 3, Application US/08766014
 Patent No. 5744312
 GENERAL INFORMATION:
 APPLICANT: Mamone, Joseph A.
 APPLICANT: Davis, Maria
 APPLICANT: Sha, Dan
 TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASE
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/766,014
 FILING DATE: Herewith
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA: including application
 PRIORITY APPLICATION DATA: described below:
 One

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/104
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 872 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-766-014-2

Query Match 45.2%; Score 38; DB 1; Length 608;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NNATYFKIDNVK 14
 Db 272 NKLEFFSLIDNIKK 285

RESULT 7
 Sequence 85, Application US/08679493A
 Patent No. 6303295
 GENERAL INFORMATION:
 APPLICANT: Taylor, Ethan W.
 TOPIC OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
 FILE REFERENCE: 55-95
 CURRENT APPLICATION NUMBER: US/08/679,493A

Query Match 45.2%; Score 38; DB 1; Length 608;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

US-08-766-014-3

CURRENT FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 60/001203
; PRIOR FILING DATE: 1995-07-14
; PRIOR APPLICATION NUMBER: 60/0003112
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 85
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-08-679-493A-85

Query Match Score 44.0%; Best Local Similarity 63.6%; Matches 7; Conservative 1; Pred. No. 45; Indels 3; Gaps 0;

QY 6 YFKIDNVKKAR 16
Db 71 YFTSDNAKQAR 81

RESULT 8
US-09-134-001C-3050
; Sequence 3050, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GIC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 3050
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3050

Query Match Score 44.0%; Best Local Similarity 87.3%; Matches 7; Conservative 0; Pred. No. 70; Indels 1; Gaps 0;

QY 5 FYFKIDNV 12
Db 174 FYFKEDNV 181

RESULT 9
US-09-282-305-14
; Sequence 14, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays

Query Match Score 44.0%; Best Local Similarity 53.3%; Matches 8; Conservative 2; Pred. No. 93; Indels 5; Gaps 0;

QY 1 NNATFYFKIDNVKK 15
Db 38 DNALMVKIDDQKLA 52

RESULT 10
US-09-282-305-12
; Sequence 12, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-282-305-12

Query Match Score 44.0%; Best Local Similarity 53.3%; Matches 8; Conservative 2; Pred. No. 94; Indels 5; Gaps 0;

QY 1 NNATFYFKIDNVKK 15
Db 38 DNALMVKIDDQKLA 52

RESULT 11
US-08-515-251A-2
; Sequence 2, Application US/08515251A
; Patent No. 5891677
; GENERAL INFORMATION:
; APPLICANT: GERLACH, GERALD F.
; APPLICANT: WILLSON, PHILIP J.
; APPLICANT: ROSSI-CAMPOS, AMALIA
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: ACTINOBACILLUS PLEUROPNEUMONIAE OUTER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/515,251A
; FILING DATE: 15 AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,558
; FILING DATE: 05-NOV-1992

ATTORNEY/AGENT INFORMATION:
 NAME: ROBINS, ROBERTA L.
 REGISTRATION NUMBER: 33, 208
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (50) 5-7812
 TELEFAX: (650) 325-7923
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-361-251A-2

Query Match 44.0%; Score 37; DB 2; Length 365;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NATFVFKTION 11
 Db 309 NGTLYSKDN 318

RESULT 12
 US-08-361-920-21
 Sequence 21, Application US/08361920
 Patent No. 5457046

GENERAL INFORMATION:
 APPLICANT: Woeldike, Helle F.
 APPLICANT: Hagen, Frederick
 APPLICANT: Hjort, Carsten M.
 APPLICANT: Sven, Hastrup
 TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/479,339
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,920
 FILING DATE: 22-DEC-1994
 APPLICATION NUMBER: US 07/940,860
 FILING DATE: 28-OCT-1992
 APPLICATION NUMBER: DK 1158/90
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00124
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 3435.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298

SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-479-939-21

Query Match 43.5%; Score 36.5; DB 1; Length 514;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

Qy 2 NATFVFKTION 14
 Db 287 NKTIVPGSNFNIDTTKK 304

RESULT 13
 US-08-479-939-21
 Sequence 21, Application US/08479939
 Patent No. 5686593

GENERAL INFORMATION:
 APPLICANT: Woeldike, Helle F.
 APPLICANT: Hagen, Frederick
 APPLICANT: Hjort, Carsten M.
 APPLICANT: Sven, Hastrup
 TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESS: No. 5686593 No. 5686593disk of No. 5686593th America, Inc.
 STREET: 405 Lexington Avenue, 62nd Floor
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10174-6201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/479,339
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/361,920
 FILING DATE: 22-DEC-1994
 APPLICATION NUMBER: US 07/940,860
 FILING DATE: 28-OCT-1992
 APPLICATION NUMBER: DK 1158/90
 FILING DATE: 09-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/DK91/00124
 FILING DATE: 08-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lambiris, Elias J.
 REGISTRATION NUMBER: 33,728
 REFERENCE/DOCKET NUMBER: 3435.204-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-867-0298

SEQUENCE CHARACTERISTICS:
 LENGTH: 514 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-479-939-21

Query Match 43.5%; Score 36.5; DB 1; Length 514;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

Qy 2 NATFVFKTION 14
 Db 287 NKTIVPGSNFNIDTTKK 304

RESULT 14
 US-08-483-432-21
 ; Sequence 21, Application US/08483432
 ; GENERAL INFORMATION:
 ; APPLICANT: Woeldeke, Helle F.
 ; APPLICANT: Hagen, Frederick
 ; APPLICANT: Hjort, Carsten M.
 ; APPLICANT: Sven, Hastrup
 ; TITLE OF INVENTION: An Enzyme Capable of Degrading Cellulose
 ; NUMBER OF SEQUENCES: 85
 ; ADDRESSEE: No 5763254 No. 5763254disk of No. 5763254th America, Inc.
 ; STREET: 405 Lexington Avenue, 62nd Floor
 ; CITY: New York
 ; STATE: United States of America
 ; COUNTRY: United States of America
 ; ZIP: 10174-6201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,432
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/361,920
 ; FILING DATE:
 ; APPLICATION NUMBER: US/07/940,860
 ; FILING DATE: 28-OCT-1992
 ; APPLICATION NUMBER: DK 1158/90
 ; FILING DATE: 09-MAY-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/DK91/00124
 ; FILING DATE: 08-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 3435.204-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-867-0298
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 514 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-483-432-21

; CURRENT APPLICATION NUMBER: US/09/230,670C
; CURRENT FILING DATE: 1998-04-05
; PRIOR APPLICATION NUMBER: PCT/EP97/04153
; PRIORITY FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-230-670C-5
Query Match Score 36.5%; DB 1; Length 514;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 4; Indels 5; Gaps 1;
Qy 2 NATFYFKIDNVKK 15
| ||| : | : | : |
Db 142 NATFWRMQYVRKS 155
Search completed: March 13 , 2003, 19:14:32
Job time : 16.3333 secs

RESULT 15
US-09-230-670C-5
; Sequence 5, Application US/09230670C
; Patent No. 6384300
; GENERAL INFORMATION:
; APPLICANT: Greiner, Steffen
; APPLICANT: Universit,t Heidelberg
; APPLICANT: Rausch, Thomas
; APPLICANT: Krausgrill, Silke
; TITLE OF INVENTION: Invertase-Inhibitor
FILE REFERENCE: 25048-13

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OM protein - protein search, using sw model

Run on: March 13, 2003, 19:12:07 ; Search time 14 Seconds
(without alignments)
52.677 Million cell updates/sec

Title: US-09-461-061a-10

Perfect score: 84

Sequence: 1 NNATYFKIDNKKAR 16

Scoring table: BLOSUM62

Gap0 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /con2_6_ptodata/1/pubpaa/pct_new_pub.pep:*

3: /cgns_6_ptodata/1/pubpaa/us06_new_pub.pep:*

4: /cgns_6_ptodata/1/pubpaa/us06_pubcomb.pep:*

5: /con2_6_ptodata/1/pubpaa/us07_new_pub.pep:*

6: /cgns_6_ptodata/1/pubpaa/us07_pubcomb.pep:*

7: /con2_6_ptodata/1/pubpaa/us08_pubcomb.pep:*

8: /cgns_6_ptodata/1/pubpaa/us09_new_pub.pep:*

9: /cgns_6_ptodata/1/pubpaa/us09_new_pub.pep:*

10: /cgns_6_ptodata/1/pubpaa/us10_new_pub.pep:*

11: /cgns_6_ptodata/1/pubpaa/us10_pubcomb.pep:*

12: /cgns_6_ptodata/1/pubpaa/us60_new_pub.pep:*

13: /cgns_6_ptodata/1/pubpaa/us60_pubcomb.pep:*

14: /cgns_6_ptodata/1/pubpaa/us60_pubcomb.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	67.9	16	10 US-09-935-682-3	Sequence 3, Appli
2	38	45.2	282	9 US-09-738-626-005	Sequence 6055, Ap
3	38	45.2	585	10 US-09-815-242-4973	Sequence 4973, Ap
4	38	45.2	586	12 US-10-010-901-40	Sequence 40, Appli
5	37	44.0	281	10 US-09-883-720-14	Sequence 14, Appli
6	37	44.0	302	10 US-09-883-720-12	Sequence 12, Appli
7	37	44.0	305	10 US-09-815-242-13653	Sequence 13653, A
8	37	44.0	359	10 US-09-815-242-13653	Sequence 376, App
9	37	44.0	717	10 US-09-801-368-376	Sequence 1463, Ap
10	36	42.9	133	10 US-09-764-877-1463	Sequence 5324, Ap
11	36	42.9	400	10 US-09-815-242-5324	Sequence 129, App
12	36	42.9	438	9 US-09-992-598-129	Sequence 129, App
13	36	42.9	438	9 US-09-989-593A-129	Sequence 129, App
14	36	42.9	438	9 US-09-989-735-129	Sequence 129, App
15	36	42.9	438	9 US-09-990-444-129	Sequence 129, App
16	36	42.9	438	9 US-09-989-730-129	Sequence 129, App
17	36	42.9	438	9 US-09-990-436-129	Sequence 129, App
18	36	42.9	438	9 US-09-991-181-129	Sequence 129, App
19	36	42.9	438	9 US-09-993-687-129	Sequence 129, App

ALIGNMENTS

RESULT 1
US-09-935-682-3

; Application US/09935682

; Sequence 3, Application US/09935682

; Patent No. US20020059032A1

; GENERAL INFORMATION:

; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques

; TITLE OF INVENTION: Rational Selection of putative Peptides from Identified Nucleo

; TITLE OF INVENTION: Peptide Sequences

; FILE REFERENCE: 58767, 0.00005

; CURRENT APPLICATION NUMBER: US/09/935, 682

; CURRENT FILING DATE: 2001-08-24

; PRIORITY APPLICATION NUMBER: 09/257, 525

; PRIORITY FILING DATE: 1999-02-25

; PRIORITY APPLICATION NUMBER: PCT/FR0/00460

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-935-682-3

RESULT 2
US-09-738-626-0055

; Sequence 6055, Application US/097388626

; Publication No. US20020197605A1

; GENERAL INFORMATION:

; APPLICANT: MIZOGUCHI, HIROSHI

; APPLICANT: ANDO, SEIKO

; APPLICANT: HAYASHI, MIKIRO

APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO: 6055
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-6055

Query Match 45.2%; Score 38; DB 10; Length 585;
Best Local Similarity 43.8%; Pred. No. 1e+02; Mismatches 3; Indels 0; Gaps 0;

RESULT 4
US-09-815-242-10580
; Sequence 10580, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; FILE REFERENCE: ELUTRA.011A
; CURRENT APPLICATION NUMBER: US/09/815, 242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 10580
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10580

Query Match 45.2%; Score 38; DB 10; Length 586;
Best Local Similarity 43.8%; Pred. No. 1e+02; Mismatches 3; Indels 0; Gaps 0;

RESULT 3
US-09-815-242-4973
; Sequence 4973, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; Prokaryotes
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206, 848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 10580
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4973

Query Match 45.2%; Score 38; DB 10; Length 586;
Best Local Similarity 43.8%; Pred. No. 1e+02; Mismatches 3; Indels 0; Gaps 0;

RESULT 5
US-10-010-901-40
; Sequence 40, Application US/10010901
; Patent No. US20020098201A1
; GENERAL INFORMATION:
; APPLICANT: McFadden, Grant
; TITLE OF INVENTION: NOVEL MYXOMA GENES FOR IMMUNE MODULATION
; FILE REFERENCE: 50082/010002
; CURRENT APPLICATION NUMBER: US/10/010,901
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/615,041
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 40
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-4973

;

LENGTH: 281

TYPE: PRT

ORGANISM: Myxoma Virus

US-10-010-901-40

RESULT 6

Query Match 44.0%; Score 37; DB 12; Length 281;
Best Local Similarity 57.1%; Pred. No. 72; Indels 0; Gaps 0;
Matches 8; Conservative 1; Mismatches 5;

Qy 1 NNATFYFKIDNYKK 14
Db 128 NVCTITFKINVSK 141

US-09-883-720-14

Sequence 14, Application US/09883720
Patent No. US200202256A1

GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718_44,
CURRENT APPLICATION NUMBER: US/09/883,720
PRIORITY APPLICATION NUMBER: 09/282,305
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 302
TYPE: PRT
ORGANISM: Zea mays

US-09-883-720-14

Query Match 44.0%; Score 37; DB 10; Length 302;
Best Local Similarity 53.3%; Pred. No. 78; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 5;

Qy 1 NNATFYFKIDNYKK 15
Db 38 DNALMYVKIDDQKLA 52

US-09-883-720-12

Sequence 12, Application US/09883720
Patent No. US200202256A1

GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718_44,
CURRENT APPLICATION NUMBER: US/09/883,720
PRIORITY APPLICATION NUMBER: 09/282,305
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 305
TYPE: PRT
ORGANISM: Zea mays

US-09-883-720-12

Query Match 44.0%; Score 37; DB 10; Length 305;
Best Local Similarity 53.3%; Pred. No. 78; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 5;

Qy 1 NNATFYFKIDNYKK 15
Db 38 DNALMYVKIDDQKLA 52

Db 38 DNALMYVKIDDQKLA 52

RESULT 8

Query Match 44.0%; Score 37; DB 10; Length 305;
Best Local Similarity 53.3%; Pred. No. 78; Indels 0; Gaps 0;

Qy 1 NNATFYFKIDNYKK 14
Db 128 NVCTITFKINVSK 141

US-09-815-242-13653

Sequence 13653, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TAXON: Prokaryotes

FILE REFERENCE: ELITRA-011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSPQ for Windows Version 4.0
SEQ ID NO 13653

Query Match 44.0%; Score 37; DB 10; Length 359;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

US-09-815-242-13653

Db 324 THYFKLSETEKA 335

RESULT 9

Query Match 44.0%; Score 37; DB 10; Length 359;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TTFYFKIDNYKK 15
Db 324 THYFKLSETEKA 335

US-09-801-368-376

Sequence 376, Application US/09801368
Patent No. US2002012850A1

GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Malone, Todd
; APPLICANT: No. US2002128250A1
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10927.147
CURRENT APPLICATION NUMBER: US/09/801,368

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; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 376
; LENGTH: 717
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-376

Query Match          44.0%; Score 37; DB 10; Length 717;
Best Local Similarity 50.0%; Pred. No. 1.9e+02; Gaps 0;
Matches 8; Conservative 2; Mismatches 6; Indels 0;
Gaps 0;

RESULT 10
US-09-764-877-1463
; Sequence 1463, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PG005
; CURRENT FILING DATE: 2001-01-17
; Prior Application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1463
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1463

Query Match          42.9%; Score 36; DB 10; Length 133;
Best Local Similarity 42.1%; Pred. No. 50; Gaps 1;
Matches 8; Conservative 5; Mismatches 2; Indels 4;
Gaps 1;

Qy   1 NNATYFKIDNVKKAR 16
      ||| :||| :||| 1
Db   255 NNAEGKLRIDNTEKDR 270

RESULT 11
US-09-815-242-5324
; Sequence 5324, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US/09/815, 242
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/207,727

Query Match          42.9%; Score 36; DB 10; Length 400;
Best Local Similarity 35.7%; Pred. No. 1.5e+02; Gaps 0;
Matches 5; Conservative 4; Mismatches 5; Indels 0;
Gaps 0;

Qy   1 NNATYFKIDNVKK 14
      ||| :||| :||| 1
Db   308 NNGDTYFRVOTIEK 321

RESULT 12
US-09-92-598-129
; Sequence 129, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klayvin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770

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PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-07-01
 PRIOR APPLICATION NUMBER: 60/091519
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091626
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091633
 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1 NNATFFKIDNVKKAR 16
 Best Local Similarity 43.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 239 NMASLYGQOLDTTKLLR 254

RESULT 13
 US-09-989-293A-129
 Sequence 129, Application US/0989293A
 Patent No. US2002017716A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Klijaviv, Ivor J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Williams, P. Mickey
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same
 FILE REFERENCE: P27301C66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-04-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089599
 PRIOR FILING DATE: 1998-06-17

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; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17 ; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/089801 ; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-06-18 ; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/089907 ; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-06-18 ; PRIOR FILING DATE: 1998-07-09

Query Match          42.9% ; Score 36; DB 9; Length 438;
Best Local Similarity 43.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 3; Mismatches 6; Indexes 0; Gaps 0;

Qy   1 NNATPFKIDNVKKAR 16
Db  239 NMASLYGQOLDTTKLR 254

RESULT 14
US-09-989-735-129
; Sequence 129, Application US/09899735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Rapoport
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber Hans Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavrin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William T.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS Encoding the Same
; FILE REFERENCE: P2730P1C161
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609

; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-06-18 ; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-06-18 ; PRIOR APPLICATION NUMBER: 60/092182
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; PRIOR FILING DATE: 1998-06-18 ; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-06-19 ; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19 ; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19 ; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19 ; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-22 ; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22 ; PRIOR APPLICATION NUMBER: 60/090252
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; PRIOR FILING DATE: 1998-06-22 ; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23 ; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23 ; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24 ; PRIOR APPLICATION NUMBER: 60/090576
; PRIOR FILING DATE: 1998-06-25 ; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25 ; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25 ; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25 ; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25 ; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01 ; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02 ; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01 ; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02 ; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02 ; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02 ;

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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
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PRIOR APPLICATION NUMBER: 60/088217
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PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/0889105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18

Query Match 42.9%; Score 36; DB 9; Length 438;
 Best Local Similarity 43.8%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 3; Mismatches 6;

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RESULT 15

US-09-990-444-129

; Sequence 129, Application US/09990444
 ; Publication No. US2002019330A1
 ; GENERAL INFORMATION:
 ; ; APPLICANT: Ashkenazi, Avi J.
 ; ; APPLICANT: Baker, Kevin P.
 ; ; APPLICANT: Botstein, David
 ; ; APPLICANT: Desnoyers, Luc
 ; ; APPLICANT: Eaton, Dan L.
 ; ; APPLICANT: Ferrara, Napoleone
 ; ; APPLICANT: Fong, Sherman
 ; ; APPLICANT: Gerber, Hanspeter
 ; ; APPLICANT: Gerritsen, Mary E.
 ; ; APPLICANT: Goddard, Audrey
 ; ; APPLICANT: Godowski, Paul J.
 ; ; APPLICANT: Grimaldi, J. Christopher
 ; ; APPLICANT: Gurney, Austin L.
 ; ; APPLICANT: Kjavian, Ivar J.
 ; ; APPLICANT: Napier, Mary A.
 ; ; APPLICANT: Pan, James
 ; ; APPLICANT: Paoni, Nicholas F.
 ; ; APPLICANT: Roy, Margaret Ann
 ; ; APPLICANT: Stewart, Timothy A.
 ; ; APPLICANT: Tumas, Daniel
 ; ; APPLICANT: Watanabe, Collin K.
 ; ; APPLICANT: Williams, P. Mickey
 ; ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: Acids Encoding the Same
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 ; CURRENT FILING DATE: 2001-11-14
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 ; PRIOR FILING DATE: 1998-07-09

Search completed: March 13, 2003, 19:15:02
 Job time : 16 secs

Query Match 42.9%; Score 36; DB 9; Length 438;
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 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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